

GenCore version 5.1.9
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 OM protein - protein search, using sw model
 Run on: September 9, 2006, 00:11:07 ; Search time 96.46 Seconds
 (without alignments)
 61.619 Million cell updates/sec

Title: US-10-797-626-1
 Perfect score: 62
 Sequence: 1 STQNASLLSLTVC 13

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8.*
 1: Geneseqp1980s.*
 2: Geneseqp1990s.*
 3: Geneseqp2000s.*
 4: Geneseqp2001s.*
 5: Geneseqp2002s.*
 6: Geneseqp2003as.*
 7: Geneseqp2003bs.*
 8: Geneseqp2004s.*
 9: Geneseqp2005s.*
 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	13	ADSL18077	Adsl18077 Laminin s
2	43	69.4	18	ADSL18079	Adsl18079 Laminin s
3	43	69.4	18	ADSL18078	Adsl18078 Laminin s
4	42	67.7	702	ADSL29055	Adsl29055 Bacterial
5	39	62.9	333	AAG79751	Aag79751 Truncated
6	39	62.9	466	ADQ76869	Adq76869 Mouse ang
7	39	62.9	469	AAV08690	Aav08690 Murine ge
8	39	62.9	580	AAV08692	Aav08692 Murine ge
9	39	62.9	812	AAV08699	Aav08699 Murine ge
10	39	62.9	812	AAV07585	Aav07585 Murine pl
11	39	62.9	812	AAV08686	Aav08686 Murine pl
12	39	62.9	812	AAV94036	Aav94036 Murine pl
13	39	62.9	812	AAV16490	Aav16490 Murine pl
14	39	62.9	812	AAV00053	Aav00053 Murine pl
15	39	62.9	812	AAV05016	Aav05016 Mouse pla
16	39	62.9	812	AAV07229	Aav07229 Amino aci
17	39	62.9	812	ABG75601	Abg75601 Mouse pla
18	39	62.9	812	AAV97950	Aav97950 Human pla
19	39	62.9	812	ADG47022	Adg47022 Murine pl
20	39	62.9	812	ADM11541	Adm11541 Murine pl
21	39	62.9	812	AED08936	Aed08936 Murine pl
22	39	62.9	812	AED64667	Aed64667 Murine pl
23	39	62.9	2000	ABR53118	Abr53118 Protein s

24	39	62.9	2000	ADK62826	ADK62826 Disease t
25	38	61.3	107	ABE89730	ABE89730 Human pol
26	37	59.7	121	AAG26056	Aag26056 Zea may
27	37	59.7	137	AAO26055	Aao26055 Zea may
28	37	59.7	292	AAO31107	Aao31107 Human mon
29	37	59.7	292	ADG29740	Adg29740 Human ADP
30	37	59.7	292	ADG29740	Adg29740 Human ADP
31	37	59.7	412	ADG67385	Adg67385 Plant ful
32	37	59.7	412	ADG67385	Adg67385 Plant ful
33	36	58.1	18	AAI16551	Aai16551 Peptide #
34	36	58.1	18	AAI16551	Aai16551 Peptide #
35	36	58.1	18	AAI16551	Aai16551 Peptide #
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97 34 54.8 326 4 AAU14511 Aau14511 Human nov 170
 98 34 54.8 326 4 AAU14275 Aau14275 Human nov 171
 99 34 54.8 326 10 AEE24185 Aee24185 Novel hum 172
 100 34 54.8 326 10 AEE23713 Aee23713 Novel hum 173
 101 34 54.8 328 8 ADH80829 Adh80829 Human pol 174
 102 34 54.8 335 5 ADP51422 Adp51422 Human MDD 175
 103 34 54.8 340 4 ABB64375 Abb64375 Drosophil 176
 104 34 54.8 370 8 ADX76442 Adx76442 Plant ful 177
 105 34 54.8 388 4 AAB82584 Aab82584 Human pro 178
 106 34 54.8 388 4 AAB82584 Aab82584 Human pro 179
 107 34 54.8 388 4 AAY72622 Aay72622 Human ang 178
 108 34 54.8 388 5 ABB77546 Abb77546 Human pol 180
 109 34 54.8 388 8 ADN12936 Adn12936 PRO19600 181
 110 34 54.8 388 8 ADN05759 Adn05759 Antipsori 182
 111 34 54.8 388 8 ADS10642 Ads10642 Human the 183
 112 34 54.8 388 8 ADS10641 Ads10641 Human the 184
 113 34 54.8 388 8 ADS10643 Ads10643 Human the 185
 114 34 54.8 388 8 ADS98865 Ads98865 Protein f 186
 115 34 54.8 388 8 ADS98867 Ads98867 Protein f 187
 116 34 54.8 388 8 ADS98866 Ads98866 Protein f 188
 117 34 54.8 391 4 AAE12467 Aae12467 Tobacco t 189
 118 34 54.8 452 5 ABP74069 Abp74069 Candida a 190
 119 34 54.8 468 3 AAG313694 Aag313694 Arabidops 191
 120 34 54.8 468 3 AAG40717 Aag40717 Zea mays 192
 121 34 54.8 473 3 AAG50305 Aag50305 Arabidops 193
 122 34 54.8 474 2 AAW22518 Aaw22518 Heat-resi 195
 123 34 54.8 477 8 ADX87404 Adx87404 Plant ful 196
 124 34 54.8 481 7 ABM85236 Abm85236 Mouse pro 197
 125 34 54.8 483 3 AAG313693 Aag313693 Arabidops 198
 126 34 54.8 483 3 AAG43982 Aag43982 Zea mays 199
 127 34 54.8 483 3 AAG43620 Aag43620 Arabidops 200
 128 34 54.8 483 3 AAG50304 Aag50304 Arabidops 201
 129 34 54.8 483 3 AAG40716 Aag40716 Zea mays 202
 130 34 54.8 488 3 AAG30457 Aag30457 Arabidops 203
 131 34 54.8 495 3 AAG50303 Aag50303 Arabidops 204
 132 34 54.8 497 8 ADX77371 Adx77371 Plant ful 205
 133 34 54.8 512 7 ABM89586 Abm89586 Rice abio 206
 134 34 54.8 512 8 ADX89374 Adx89374 Plant ful 207
 135 34 54.8 528 3 AAG313692 Aag313692 Arabidops 208
 136 34 54.8 528 8 ADN73329 Adn73329 Thale cre 209
 137 34 54.8 529 3 AAG43981 Aag43981 Zea mays 210
 138 34 54.8 532 3 AAG43619 Aag43619 Arabidops 211
 139 34 54.8 533 8 ADMA48281 Adm48281 Polypepti 212
 140 34 54.8 534 3 AAG40715 Aag40715 Zea mays 213
 141 34 54.8 539 8 ADX93379 Adx93379 Plant ful 214
 142 34 54.8 539 8 ADX93332 Adx93332 Plant ful 215
 143 34 54.8 543 3 AAG30456 Aag30456 Arabidops 216
 144 34 54.8 565 3 AAG43980 Aag43980 Zea mays 217
 145 34 54.8 585 3 AAG43618 Aag43618 Arabidops 218
 146 34 54.8 624 5 ABP73960 Abp73960 Candida a 219
 147 34 54.8 658 8 ADY07300 Ady07300 Plant ful 220
 148 34 54.8 693 4 ABB61294 Abb61294 Drosophil 221
 149 34 54.8 693 10 AEG02520 Aeg02520 Drosophil 222
 150 34 54.8 743 8 ADJ25684 Adj25684 Human BAB 223
 151 34 54.8 767 5 ABP69549 Abp69549 Human pol 224
 152 34 54.8 849 4 ABG29195 Abg29195 Novel hum 225
 153 34 54.8 924 4 ABG25678 Abg25678 Novel hum 226
 154 34 54.8 1033 8 ADJ25714 Adj25714 Full leng 227
 155 34 54.8 1145 8 ADY22672 Ady22672 Plant ful 228
 156 34 54.8 1184 4 ABG20726 Abg20726 Novel hum 229
 157 34 54.8 1266 4 ABB68444 Abb68444 Drosophil 230
 158 34 54.8 1456 2 AAR24033 Aar24033 Soluble m 231
 159 34 54.8 1456 6 ABU79121 Abu79121 Angiostat 232
 160 34 54.8 1456 7 ADF43375 Adf43375 Mamose r 233
 161 34 54.8 1456 7 ADN39899 Adn39899 Cancer/an 234
 162 34 54.8 1456 7 ADN95147 Adn95147 Human BEC 235
 163 34 54.8 1456 8 ADL12439 Adl12439 Human ste 236
 164 34 54.8 1456 8 ADQ17856 Adq17856 Human sof 237
 165 34 54.8 1456 8 ADP23714 Adp23714 PRO polyp 238
 166 34 54.8 1456 9 AEA03046 Aea03046 Glycophor 239
 167 34 54.8 17 10 AEF43274 Aef43274 Human Mul 240
 168 34 53.2 18 10 AEF43275 Aef43275 Human Mul 241
 169 34 53.2 19 9 ADX56211 Adx56211 Cardiovas 242

19 9 ADY38279 Ady38279 Human CPP 170
 20 10 AEF43226 Aef43226 Human Mul 171
 21 10 AEF43227 Aef43227 Human Mul 172
 22 2 AAW88566 Aaw88566 Secreted 173
 23 2 ABB50333 Abb50333 Human sec 174
 24 6 ABO44590 Abo44590 Novel hum 175
 25 7 ABO26070 Abo26070 Human pro 176
 26 32 AAB36406 Aab36406 Human sec 177
 27 4 AAU01625 Aau01625 Human pro 178
 28 4 AAM16375 Aam16375 Peptide # 179
 29 4 ABB35363 Abb35363 Peptide # 180
 30 4 AAM28872 Aam28872 Peptide # 181
 31 4 ABB30200 ABB30200 Peptide # 182
 32 4 ABB20805 Aab20805 Protein # 183
 33 4 AAM68567 Aam68567 Human bon 184
 34 4 AAM56194 Aam56194 Human bra 185
 35 4 AAG50230 Aag50230 Human liv 186
 36 4 AAM04111 Aam04111 Peptide # 187
 37 4 AAG38145 Aag38145 Human pep 188
 38 4 AAU71978 Aau71978 Human bon 189
 39 4 AAO04908 Aao04908 Human pol 190
 40 65 10 AEF87491 Aef87491 Glycosyls 191
 41 2 AAW88640 Aaw88640 Secreted 192
 42 2 ABB50407 Abo50407 Human sec 193
 43 6 ABO44664 Abo44664 Novel hum 194
 44 7 ABO26144 Abo26144 Human pro 195
 45 4 AAU51335 Aau51335 Propionib 196
 46 6 ABM47854 Abm47854 Propionib 197
 47 73 6 AAU43704 Aau43704 Propionib 198
 48 76 4 AAM40223 Aam40223 Propionib 199
 49 76 9 AEB39767 Aeb39767 L. pneumo 200
 50 77 3 AAB22815 Aab22815 Human pla 201
 51 89 7 ADC27561 Adc27561 Human col 202
 52 91 9 AEB36350 Aeb36350 L. pneumo 203
 53 99 4 AEG24120 Aeg24120 Novel hum 204
 54 105 9 AEC81781 Aec81781 Human imm 205
 55 110 8 AEX80301 Aex80301 Plant ful 206
 56 120 2 AAY59781 Aay59781 Human nor 207
 57 120 2 AAY60507 Aay60507 Human nor 208
 58 121 3 AAY95725 Aay95725 Cosmid ch 209
 59 128 4 AEG24121 Aeg24121 Novel hum 210
 60 130 4 AAG72604 Aag72604 Human OR- 211
 61 133 5 AAG78462 Aag78462 Mouse Ig- 212
 62 142 4 AAG90684 Aag90684 C. glutami 213
 63 142 7 ADL66005 Aef66005 C. glutam 214
 64 164 10 AEF20612 Aef20612 Human ost 215
 65 172 3 AAY74453 Aay74453 Neisseria 216
 66 172 6 ABP78992 Abp78992 N. gonorr 217
 67 186 7 ADB63992 Adb63992 Human pro 218
 68 189 4 AAB36411 Aab36411 Human sec 219
 69 198 3 AAG29409 Aag29409 Arabidops 220
 70 200 7 ADR69832 Adr69832 Wild-type 221
 71 200 7 ADR69830 Adr69830 Synthetic 222
 72 200 7 ADR69853 Adr69853 Wild-type 223
 73 200 7 ADR69839 Adr69839 Wild-type 224
 74 200 7 ADR69900 Adr69900 Synthetic 225
 75 205 7 ADJ71112 Adj71112 Human hea 226
 76 205 8 ADN99452 Adn99452 Novel hum 227
 77 212 3 AAG29408 Aag29408 Arabidops 228
 78 213 8 ABO60120 Abo60120 Human gen 229
 79 228 2 AAR27282 Aar27282 B cell re 230
 80 228 2 AAR78672 Aar78672 B29 recep 231
 81 228 2 AAW02219 Aaw02219 B cell re 232
 82 228 2 AAW83146 Aaw83146 B29 recep 233
 83 228 2 AAG29407 Aag29407 Arabidops 234
 84 5 ABB53729 Abb53729 Mouse imm 235
 85 244 5 ABB55339 Abb55339 Lactococc 236
 86 244 8 ADI62537 Adi62537 Murine SF 237
 87 244 8 ADI62537 Adi62537 Murine SF 238
 88 245 3 AAG43329 Aag43329 Arabidops 239
 89 245 3 AAG04549 Aag04549 Arabidops 240
 90 255 9 AEC31757 Aec31757 Human LRH 241

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:25:14 ; Search time 15.6 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-797-626-1

Perfect score: 62

Sequence: 1 STQNALLSLTVC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	67.7	326	1 VGXRVA	glycoprotein VP7 p
2	40	64.5	326	1 A48554	glycoprotein VP7 p
3	40	64.5	326	1 VGXRMI	glycoprotein VP7 p
4	40	64.5	326	1 VGXRNI	glycoprotein VP7 p
5	40	64.5	531	2 C97141	site-specific reco
6	39	62.9	812	1 PLMS	plasma (EC 3.4.21
7	39	62.9	2493	2 S45734	probable membrane
8	37	59.7	601	2 T11677	probable transcrip
9	36	58.1	326	1 VGXRK4	glycoprotein VP7 p
10	36	58.1	560	2 S27874	steroid hormone re
11	36	58.1	812	1 PLBO	plasma (EC 3.4.21
12	36	58.1	1313	2 T38943	probable guanine n
13	36	58.1	6805	2 S20901	titin - rabbit (fr
14	35	57.3	604	2 T15514	hypothetical prote
15	35	56.5	100	2 FN0619	hypothetical prote
16	35	56.5	115	2 S74763	hypothetical prote
17	35	56.5	211	2 A85098	hypothetical prote
18	35	56.5	211	2 C84775	probable harpin-in
19	35	56.5	326	1 VGXRAG	glycoprotein VP7 p
20	35	56.5	333	1 VHNZPM	nucleocapsid prote
21	35	56.5	456	2 G83449	probable MFS trans
22	35	56.5	718	2 F90512	hypothetical prote
23	34	54.8	62	2 C81101	hypothetical prote
24	34	54.8	120	2 A72617	hypothetical prote
25	34	54.8	179	2 AF0553	probable lipoprote
26	34	54.8	186	2 T16056	hypothetical prote
27	34	54.8	245	2 E87719	protein R19.3 (im
28	34	54.8	262	2 AB1196	enoyl- acyl-carrie
29	34	54.8	262	2 AB11553	enoyl- acyl-carrie

30	54.8	293	2	E83513	probable outer mem
31	54.8	308	2	T26007	hypothetical prote
32	54.8	391	2	S22579	translation initia
33	54.8	407	2	T06824	translation initia
34	54.8	468	1	B46114	glycoprotein gp13
35	54.8	468	1	VGEEEH	glycoprotein gp13
36	54.8	492	2	A02993	succinoglycan bios
37	54.8	493	2	F98290	exor protein (limp
38	54.8	543	2	F96624	hypothetical prote
39	54.8	551	2	B88949	protein R09B5.4 [i
40	54.8	573	2	C82525	hypothetical prote
41	54.8	1456	1	A36563	mannose receptor p
42	54.8	2048	1	ZLNZSE	genome polyprotein
43	54.8	2228	1	ZLNZSV	plasma (EC 3.4.21
44	54.8	120	2	E61545	orf6 protein - Aut
45	53.2	121	2	F44221	plasma (EC 3.4.21
46	53.2	123	2	C61545	hypothetical prote
47	53.2	131	2	A84448	hypothetical prote
48	53.2	197	2	A82571	hypothetical prote
49	53.2	228	2	E86253	hypothetical prote
50	53.2	228	2	A31403	membrane protein B
51	53.2	244	2	A86873	transcription regu
52	53.2	257	2	C86784	pseudouridine synt
53	53.2	261	2	B86643	carbonyl reductase
54	53.2	279	2	T21099	hypothetical prote
55	53.2	312	2	T05529	magnesium-protopor
56	53.2	326	1	VGXRWL	glycoprotein VP7 p
57	53.2	326	2	JC4196	36K hydrophobic nu
58	53.2	327	2	JC4195	36K hydrophobic nu
59	53.2	399	2	D86460	F14M2.17 protein -
60	53.2	425	2	E88115	protein F53C3.11 [
61	53.2	428	1	EHHU	ig epsilon chain C
62	53.2	439	2	C94981	hypothetical prote
63	53.2	460	2	B61545	plasma (EC 3.4.21
64	53.2	461	1	A46077	steroid hormone re
65	53.2	461	2	JC4972	steroidogenic fact
66	53.2	462	1	A56120	steroid hormone re
67	53.2	462	2	A40716	steroid hormone re
68	53.2	464	2	E99103	protein C18B10.4 [
69	53.2	464	2	A53101	vitamin D3 hydroxy
70	53.2	478	2	E90930	hypothetical prote
71	53.2	478	2	A85779	hypothetical prote
72	53.2	478	2	B64929	hypothetical prote
73	53.2	480	2	AF0704	conserved hypotet
74	53.2	501	1	A56543	Ftz-F1-related orp
75	53.2	519	2	D82536	conserved hypotet
76	53.2	535	2	D86680	hypothetical prote
77	53.2	623	2	T29139	hypothetical prote
78	53.2	644	2	T47835	hypothetical prote
79	53.2	714	2	E82507	hypothetical prote
80	53.2	740	2	T12223	NADH2 dehydrogenas
81	53.2	747	2	S66959	hypothetical prote
82	53.2	784	2	T43510	probable spindle p
83	53.2	810	1	PLHU	plasma (EC 3.4.21
84	53.2	1012	2	B73326	endoglucanase fami
85	53.2	1042	2	T13647	hypothetical prote
86	53.2	1208	2	S69015	AXL1 protein - yea
87	53.2	1252	2	S36016	oocyst wall protei
88	53.2	1357	2	B96696	protein FIN21.4 [i
89	53.2	1433	2	S54587	CAR8 protein - yea
90	53.2	1455	1	A48925	mannose receptor p
91	53.2	2102	2	T15626	hypothetical prote
92	53.2	2351	2	G71415	hypothetical prote
93	53.2	3295	2	AE0074	probable adhesin y
94	53.2	33	2	D61545	plasma (EC 3.4.21
95	51.6	49	2	JH0641	rab protein Rab5c
96	51.6	160	2	F86283	protein T15D22.6 [
97	51.6	208	2	T21442	hypothetical prote
98	51.6	215	2	F34323	GTP-binding protei
99	51.6	215	2	A30413	GTP-binding protei
100	51.6	216	2	I38703	ras-related small
101	51.6	216	2	S65933	GTP-binding protei
102	51.6	251	2	T32318	hypothetical prote

103	32	51.6	275	1	RGBV7K	mitochondrial impo	176	31	50.0	326	1	VGXRCB	glycoprotein VP7 p
104	32	51.6	298	2	T33220	hypothetical prote	177	31	50.0	326	1	VGXRDB	glycoprotein VP7 p
105	32	51.6	326	1	VGXRRL	glycoprotein VP7 p	178	31	50.0	326	1	S25546	outer capsid prote
106	32	51.6	326	1	VGXRRL	glycoprotein VP7 p	179	31	50.0	326	1	H70782	probable ompA prot
107	32	51.6	326	1	VGXRRL	glycoprotein VP7 p	180	31	50.0	327	2	B69856	oligopeptide trans
108	32	51.6	329	2	T43509	probable potassium	181	31	50.0	341	2	S55627	hypothetical prote
109	32	51.6	336	2	A10645	probable virulence	182	31	50.0	369	2	F70905	probable lipoprote
110	32	51.6	336	2	T23247	outward refuclier	183	31	50.0	374	2	T50265	probable phosphate
111	32	51.6	367	2	AD0063	hypothetical prote	184	31	50.0	381	2	F71078	hypothetical prote
112	32	51.6	381	2	B13701	NADH2 dehydrogenas	185	31	50.0	388	1	VCVGAC	coat protein - art
113	32	51.6	381	2	B82420	conserved hypotet	186	31	50.0	413	2	H95041	polysaccharide tra
114	32	51.6	384	2	T29787	hypothetical prote	187	31	50.0	428	2	T28007	hypothetical prote
115	32	51.6	404	2	AC3357	molybdopterin bios	188	31	50.0	430	2	T19556	hypothetical prote
116	32	51.6	405	2	T25320	hypothetical prote	189	31	50.0	437	1	F64782	probable transport
117	32	51.6	427	2	B71466	hypothetical prote	190	31	50.0	439	2	T52304	phytochrome kinase
118	32	51.6	448	2	A27522	UDP-N-acetylglucos	191	31	50.0	439	2	E84442	hypothetical prote
119	32	51.6	449	2	E70016	purine permease ho	192	31	50.0	443	2	H87911	protein B0205.4 li
120	32	51.6	539	2	H82994	probable permease	193	31	50.0	446	2	S26965	NADH oxidase - Ent
121	32	51.6	564	2	T40883	WD repeat protein	194	31	50.0	448	2	AH0916	probable regulator
122	32	51.6	660	2	T22794	hypothetical prote	195	31	50.0	448	2	A38445	EV12B protein prec
123	32	51.6	675	2	B90000	hypothetical prote	196	31	50.0	463	2	D90700	probable transport
124	32	51.6	679	2	S02165	regulatory protein	197	31	50.0	463	2	G85550	probable transport
125	32	51.6	688	2	S65241	hypothetical prote	198	31	50.0	465	2	T27580	hypothetical prote
126	32	51.6	694	2	T33561	hypothetical prote	199	31	50.0	466	2	F88843	protein ZK809.1 li
127	32	51.6	711	2	T12628	NADH2 dehydrogenas	200	31	50.0	475	2	D86651	polysaccharide bio
128	32	51.6	765	2	T46178	hypothetical prote	201	31	50.0	487	2	T02719	permease 1 - maize
129	32	51.6	817	2	T51787	hypothetical prote	202	31	50.0	489	2	S69027	ammonium transport
130	32	51.6	954	2	A74731	regulatory protein	203	31	50.0	489	2	T04596	hypothetical prote
131	32	51.6	1005	2	A42265	alpha-mannosidase	204	31	50.0	502	2	A56683	receptor protein k
132	32	51.6	1011	2	T13055	dynamain associated	205	31	50.0	502	2	A53444	activin receptor-1
133	32	51.6	1088	2	T14317	homeotic protein p	206	31	50.0	502	2	JC2491	serine/threonine k
134	32	51.6	1094	2	T13053	dynamain associated	207	31	50.0	505	2	F90427	amino acid transpo
135	32	51.6	1101	2	T33153	hypothetical prote	208	31	50.0	510	1	DERZ2	NADH2 dehydrogenas
136	32	51.6	1178	2	S57698	regulatory protein	209	31	50.0	510	2	S65076	NADH2 dehydrogenas
137	32	51.6	1227	2	A86245	hypothetical prote	210	31	50.0	510	2	S38992	NADH2 dehydrogenas
138	32	51.6	1247	2	T18671	hypothetical prote	211	31	50.0	518	2	T05196	hypothetical prote
139	32	51.6	1699	2	T14074	complement compone	212	31	50.0	568	2	T34522	hypothetical prote
140	32	51.6	2232	2	T34434	hypothetical prote	213	31	50.0	574	2	C86400	hypothetical prote
141	32	51.6	2895	2	H85362	hypothetical prote	214	31	50.0	606	2	T11412	NADH2 dehydrogenas
142	32	51.6	3591	1	S21010	filamentous hemagg	215	31	50.0	625	2	AD2251	two-component sens
143	32	51.6	4466	1	S17231	dynein beta heavy	216	31	50.0	628	2	A84649	probable glucose r
144	32	51.6	4466	1	S17653	dynein beta heavy	217	31	50.0	628	2	A84649	transforming prote
145	31	50.0	67	2	A71808	hypothetical prote	218	31	50.0	686	1	S28050	NADH2 dehydrogenas
146	31	50.0	94	2	T03751	hypothetical prote	219	31	50.0	698	2	T12586	NADH2 dehydrogenas
147	31	50.0	98	2	S70598	NADH2 dehydrogenas	220	31	50.0	699	2	T13730	NADH2 dehydrogenas
148	31	50.0	101	2	I46871	hypothetical prote	221	31	50.0	727	2	T44920	heterocyst-specifi
149	31	50.0	109	2	C81993	hypothetical prote	222	31	50.0	727	2	AC1908	heterocyst-specifi
150	31	50.0	118	2	C64441	conserved hypotet	223	31	50.0	849	2	T19878	hypothetical prote
151	31	50.0	119	2	D81221	hypothetical prote	224	31	50.0	926	2	H88226	hypothetical prote
152	31	50.0	124	2	S50379	hypothetical prote	225	31	50.0	926	2	H88226	hypothetical prote
153	31	50.0	141	2	T33983	hypothetical prote	226	31	50.0	971	2	T39912	conserved hypotet
154	31	50.0	146	2	T32255	hypothetical prote	227	31	50.0	971	2	T39912	protein C41C4.5 (i
155	31	50.0	160	2	H64595	hypothetical prote	228	31	50.0	1012	2	T09339	protein C41C4.5 (i
156	31	50.0	164	2	T36486	hypothetical prote	229	31	50.0	1025	2	G85834	conserved hypotet
157	31	50.0	183	2	D45332	orf4 protein - por	230	31	50.0	1025	2	G85834	hypothetical prote
158	31	50.0	183	2	S36861	orf4 protein - lel	231	31	50.0	1025	2	G85834	hypothetical prote
159	31	50.0	189	2	S53299	ribonuclease (EC 3	232	31	50.0	1025	2	C84974	hypothetical prote
160	31	50.0	199	2	S76292	hypothetical prote	233	31	50.0	1025	2	AC3568	hypothetical prote
161	31	50.0	210	2	S66484	insulin-like growt	234	31	50.0	1026	2	AE0771	hypothetical prote
162	31	50.0	225	2	C88633	protein P56B3.3 li	235	31	50.0	1029	2	T05050	probable RND-famil
163	31	50.0	229	2	A46527	B-cell-specific me	236	31	50.0	1097	2	J03031	protein kinase hom
164	31	50.0	242	2	AB0719	probable percutis	237	31	50.0	1548	1	DVLNS	multidrug resistan
165	31	50.0	246	2	AE0153	probable Laci-fami	238	31	50.0	1636	2	B82736	hemolysin-type cal
166	31	50.0	257	2	A02991	myosin heavy chain	239	31	50.0	1902	2	S06997	lactococpin (EC 3.4
167	31	50.0	266	2	AB0060	probable membrane	240	31	50.0	1902	2	B45764	lactococpin (EC 3.4
168	31	50.0	267	2	T33911	hypothetical prote	241	31	50.0	1962	2	A32634	hypothetical prote
169	31	50.0	293	2	T27598	hypothetical prote	242	30.5	49.2	452	2	T02492	hypothetical prote
170	31	50.0	295	2	AE1318	probable lipid A b	243	30.5	49.2	807	2	AC1031	hypothetical prote
171	31	50.0	297	2	AF3651	transcription regu	244	30	48.4	90	1	RHMSG	gonadoliberin prec
172	31	50.0	299	2	T29539	hypothetical prote	245	30	48.4	96	2	T07136	probable metalloca
173	31	50.0	310	2	T32677	hypothetical prote	246	30	48.4	96	2	T07136	probable metalloca
174	31	50.0	320	2	T47882	hypothetical prote	247	30	48.4	98	2	A28918	hypothetical prote
175	31	50.0	326	1	VGXR66	glycoprotein VP7 p	248	30	48.4	106	2	AC0430	primosomal replica

GenCore version 5.1.9
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 OM protein - protein search, using sw model
 Run on: September 9, 2006, 00:11:36 ; Search time 129.74 Seconds
 (without alignments)
 92.687 Million cell updates/sec
 Title: US-10-797-626-1
 Perfect score: 62
 Sequence: 1 STQNASLLSLTVC 13
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 2849598 seqs, 925015592 residues
 Total number of hits satisfying chosen parameters: 2849598
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries
 Database : Uniprot 7.2.*
 1: uniprot_sprot.*
 2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	69.4	254	2	Q7THM5_9REOV
2	43	69.4	263	2	Q8QU19_9REOV
3	42	67.7	254	2	Q7THM3_9REOV
4	42	67.7	254	2	Q7THM4_9REOV
5	42	67.7	326	1	VS09_ROTUV
6	42	67.7	326	2	Q86258_9REOV
7	42	67.7	326	2	Q86268_9REOV
8	42	67.7	326	2	Q86269_9REOV
9	42	67.7	326	2	Q9QC23_9REOV
10	42	67.7	702	2	Q9HM26_9REOV
11	40	64.5	84	2	Q6LSA1_PHOPE
12	40	64.5	263	2	Q8QU18_9REOV
13	40	64.5	263	2	Q8QU20_9REOV
14	40	64.5	263	2	Q8QU21_9REOV
15	40	64.5	263	2	Q8QU22_9REOV
16	40	64.5	263	2	Q8QU23_9REOV
17	40	64.5	263	2	Q8QU24_9REOV
18	40	64.5	263	2	Q8QU25_9REOV
19	40	64.5	263	2	Q8QU26_9REOV
20	40	64.5	263	2	Q8QU27_9REOV
21	40	64.5	263	2	Q8QU28_9REOV
22	40	64.5	263	2	Q8QU29_9REOV
23	40	64.5	263	2	Q8QU30_9REOV
24	40	64.5	263	2	Q8QU31_9REOV
25	40	64.5	263	2	Q8QU32_9REOV
26	40	64.5	263	2	Q8QU33_9REOV
27	40	64.5	263	2	Q8QU34_9REOV
28	40	64.5	263	2	Q8QU35_9REOV
29	40	64.5	263	2	Q8QU36_9REOV
30	40	64.5	263	2	Q8QU37_9REOV
31	40	64.5	326	1	VS09_ROTUV

32	40	64.5	326	1	VS09_ROTUV	P27423 porcine rot
33	40	64.5	326	1	VS09_ROTUV	P32549 porcine rot
34	40	64.5	326	2	Q783Y5_9REOV	Q783Y5 human rotav
35	40	64.5	326	2	Q786Y4_9REOV	Q786Y4 human rotav
36	40	64.5	326	2	Q8B3A0_9REOV	Q8B3A0 human rotav
37	40	64.5	326	2	Q9PX10_9REOV	Q9PX10 human rotav
38	40	64.5	326	2	Q9PX98_9REOV	Q9PX98 human rotav
39	40	64.5	326	2	Q9QGR4_9REOV	Q9QGR4 human rotav
40	40	64.5	326	2	Q9QGR5_9REOV	Q9QGR5 human rotav
41	40	64.5	531	2	Q97HQ2_CLOAB	Q97HQ2 clostridium
42	40	64.5	1816	2	Q4RPB4_TETNG	Q4RPB4 tetraodon n
43	39	62.9	254	2	Q7THM6_9REOV	Q7THM6 porcine rot
44	39	62.9	254	2	Q7THM7_9REOV	Q7THM7 porcine rot
45	39	62.9	326	2	Q6LSY6_9REOV	Q6LSY6 porcine rot
46	39	62.9	466	2	Q6TC10_MOUSE	Q6TC10 mus musculus
47	39	62.9	812	1	PLMN_MOUSE	P20918 mus musculus
48	39	62.9	812	2	Q3V1T9_MOUSE	Q3V1T9 mus musculus
49	39	62.9	2493	1	YBA4_YEAST	P35194 saccharomyc
50	38	61.3	84	2	Q8JYM8_9REOV	Q8JYM8 bovine rota
51	38	61.3	94	2	Q37389_CCPV1	Q37389 common chim
52	38	61.3	119	2	Q5APL2_CANAL	Q5APL2 candida alb
53	38	61.3	172	2	Q7PX25_ANOGA	Q7PX25 anopheles g
54	38	61.3	214	2	Q567N4_BRARE	Q567N4 brachydanio
55	38	61.3	229	2	Q6M9T8_PARUM	Q6M9T8 parachlamyd
56	38	61.3	284	2	Q2VSHI_9GAMA	Q2VSHI ovine herpe
57	38	61.3	396	2	Q510M0_ENTHI	Q510M0 entamoeba h
58	38	61.3	593	2	Q71S51_9ECHI	Q71S51 ophiopholis
59	38	61.3	1575	2	Q8SSN3_DICDI	Q8SSN3 dictyosteli
60	37	59.7	180	2	Q95KT4_MACMU	Q95KT4 macaca mula
61	37	59.7	185	2	Q5ORL7_ENTHI	Q5ORL7 entamoeba h
62	37	59.7	203	2	Q4TIB6_TETNG	Q4TIB6 tetraodon n
63	37	59.7	215	2	Q2XKP2_PSEPU	Q2XKP2 pseudomonas
64	37	59.7	215	2	Q88GY6_PSEPK	Q88GY6 pseudomonas
65	37	59.7	254	2	Q7THM2_9REOV	Q7THM2 porcine rot
66	37	59.7	292	1	NAR5_HUMAN	Q96115 homo sapien
67	37	59.7	292	2	Q86W02_HUMAN	Q86W02 homo sapien
68	37	59.7	326	2	Q56663_9REOV	Q56663 rotavirus g
69	37	59.7	326	2	Q86508_9REOV	Q86508 rotavirus
70	37	59.7	330	2	Q5JBB0_HYMNA	Q5JBB0 hymenocalli
71	37	59.7	401	2	Q5CZT0_BRARE	Q5CZT0 brachydanio
72	37	59.7	407	2	Q2MJJ9_WAIZE	Q2MJJ9 zea mays (m
73	37	59.7	409	2	Q4T9R3_TETNG	Q4T9R3 tetraodon n
74	37	59.7	430	2	Q4UC32_THEAN	Q4UC32 theileria a
75	37	59.7	460	2	Q88EP6_PSEPK	Q88EP6 pseudomonas
76	37	59.7	572	2	Q2XER1_PSEPU	Q2XER1 pseudomonas
77	37	59.7	601	1	UCP3_SCHPO	Q74345 schizosacch
78	37	59.7	795	2	Q5B8S6_EMENI	Q5B8S6 aspergillus
79	37	59.7	1110	2	Q4IA83_GIBZE	Q4IA83 gibberella
80	37	59.7	2228	1	L_SENDA	Q9dud8 sendai viru
81	37	59.7	2228	1	L_SENDO	Q55528 sendai viru
82	37	59.7	2229	2	Q3KGS5_9PARA	Q3KGS5 sendai viru
83	37	59.7	6781	1	RIAB_PEDV7	Q91av2 p replicase
84	36	58.1	84	2	Q8JYM3_9REOV	Q8JYM3 bovine rota
85	36	58.1	84	2	Q8JYM6_9REOV	Q8JYM6 bovine rota
86	36	58.1	84	2	Q8JYN7_9REOV	Q8JYN7 bovine rota
87	36	58.1	131	2	Q9PUJ7_ALLMI	Q9PUJ7 alligator m
88	36	58.1	147	2	Q8XP98_CLOPE	Q8XP98 clostridium
89	36	58.1	153	2	Q5X4H1_LEGPA	Q5X4H1 legionella
90	36	58.1	221	2	Q4CSL9_TRYCR	Q4CSL9 trypanosoma
91	36	58.1	224	2	Q8B313_9REOV	Q8B313 human rotav
92	36	58.1	280	2	Q68QF8_9REOV	Q68QF8 bovine rota
93	36	58.1	293	2	Q61S86_CAEBR	Q61S86 caenorhabdi
94	36	58.1	299	2	Q5LEJ7_BACFN	Q5LEJ7 bacteroides
95	36	58.1	299	2	Q91E85_9REOV	Q91E85 human rotav
96	36	58.1	318	2	Q6MSW8_MYCMS	Q6MSW8 mycoplasma
97	36	58.1	326	1	VS07_ROTUV	P31632 bovine rota
98	36	58.1	326	2	Q45NQ0_9REOV	Q45NQ0 human rotav
99	36	58.1	326	2	Q65698_9REOV	Q65698 bovine rota
100	36	58.1	326	2	Q6WKW7_9REOV	Q6WKW7 buffalo rot
101	36	58.1	326	2	Q77LU9_9REOV	Q77LU9 canine rota
102	36	58.1	326	2	Q783Y8_9REOV	Q783Y8 human rotav
103	36	58.1	326	2	Q786Y6_9REOV	Q786Y6 human rotav
104	36	58.1	326	2	Q808C2_9REOV	Q808C2 human rotav

105	36	58.1	326	2	Q80AQ3_9REOV	Q80aq3 rabbit rota	178	35	56.5	326	2	Q9E3U7_9REOV	Q9e3u7 human rotav
106	36	58.1	326	2	Q82018_9REOV	Q82018 human rotav	179	35	56.5	326	2	Q9ID00_9REOV	Q9id00 human rotav
107	36	58.1	326	2	Q86212_9REOV	Q86212 human rotav	180	35	56.5	326	2	Q9IG14_9REOV	Q9ig14 human rotav
108	36	58.1	326	2	Q86270_9REOV	Q86270 rotavirus s	181	35	56.5	326	2	Q9QTF5_9REOV	Q9qtf5 human rotav
109	36	58.1	326	2	Q86271_9REOV	Q86271 rotavirus s	182	35	56.5	326	2	Q9QTF6_9REOV	Q9qtf6 human rotav
110	36	58.1	326	2	Q8B399_9REOV	Q8b399 human rotav	183	35	56.5	326	2	Q9W893_9REOV	Q9w893 human rotav
111	36	58.1	326	2	Q8B314_9REOV	Q8b314 human rotav	184	35	56.5	326	2	Q9W899_9REOV	Q9w899 human rotav
112	36	58.1	326	2	Q8B316_9REOV	Q8b316 human rotav	185	35	56.5	326	2	Q9W900_9REOV	Q9w900 human rotav
113	36	58.1	326	2	Q8JLW9_9REOV	Q8jlw9 caprine rot	186	35	56.5	326	2	Q9W911_9REOV	Q9w911 human rotav
114	36	58.1	326	2	Q917F2_9REOV	Q917f2 human rotav	187	35	56.5	326	2	Q9B960_9PEZI	Q9b960 galiella ru
115	36	58.1	326	2	Q9PWU5_9REOV	Q9pwu5 human rotav	188	35	56.5	326	2	Q3NVH0_9GAMM	Q3nyh0 shewanella
116	36	58.1	326	2	Q9Q3G1_9REOV	Q9q3g1 human rotav	189	35	56.5	326	2	Q9TFV3_9SAUR	Q9tfv3 teratocinc
117	36	58.1	326	2	Q9Q3G2_9REOV	Q9q3g2 human rotav	190	35	56.5	326	2	Q50YU9_ENTHI	Q50y9 entameoba h
118	36	58.1	326	2	Q9QPS6_9REOV	Q9qps6 rotavirus a	191	35	56.5	326	2	NCAP_MPVI5	Q50y9 murine pneu
119	36	58.1	326	2	Q3T324_9HIV1	Q3t324 human immun	192	35	56.5	326	2	Q50EV9_9MONO	Q50ev9 pneumonia v
120	36	58.1	326	2	Q2SLT0_9GAMM	Q2slt0 hahella che	193	35	56.5	326	2	Q5MKP0_9MONO	Q5mkp0 pneumonia v
121	36	58.1	326	2	Q8WE19_9SAUR	Q8we19 draco bosch	194	35	56.5	326	2	Q6PWL2_9MONO	Q6pwl2 enterococu
122	36	58.1	326	2	Q2QJ3_9ECHI	Q2qj3 phanogenia	195	35	56.5	326	2	Q833B2_ENTFA	Q833b2 trypanosoma
123	36	58.1	326	2	Q6N1R4_CORDI	Q6ni4 corynebacte	196	35	56.5	326	2	Q387C8_9TRYP	Q387c8 chlorobium
124	36	58.1	326	2	Q9NAV8_CAEEL	Q9nav8 caenorhabdi	197	35	56.5	326	2	Q3AQR8_CHLCH	Q3aqr8 pseudomonas
125	36	58.1	326	2	Q4HMB1_CAMELA	Q4hmb1 campylobact	198	35	56.5	326	2	Q913B8_PSEAE	Q913b8 pseudomonas
126	36	58.1	326	2	Q8A3P1_BACTN	Q8a3p1 bacteroides	199	35	56.5	326	2	Q9Y154_TRASC	Q9y154 trachemys s
127	36	58.1	326	2	Q7PNT6_ANOGA	Q7pnt6 anopheles g	200	35	56.5	326	2	Q9BHF5_LEIMA	Q9bhf5 leishmania
128	36	58.1	326	2	Q42102_CHICK	Q42102 gallus gall	201	35	56.5	326	2	Q4ZYG6_PSEU2	Q4zyg6 pseudomonas
129	36	58.1	326	2	Q90XC4_POEGU	Q90xc4 poephila qu	202	35	56.5	326	2	Q4WFB5_ASPFU	Q4wfb5 aspergillus
130	36	58.1	326	2	Q9PMI7_CHICK	Q9pmi7 gallus gall	203	35	56.5	326	2	Q2WH28_CLOBE	Q2wh28 clostridium
131	36	58.1	326	2	NR5A2_MOUSE	P45448 mus musculus	204	35	56.5	326	2	Q2S206_9SPHI	Q2s206 salinibacte
132	36	58.1	326	2	Q2L3D5_BRASY	Q2l3d5 brachypodiu	205	35	56.5	326	2	Q5QR21_NOTTY	Q5qr21 notoryctes
133	36	58.1	326	2	Q4PCF8_USTMA	Q4pcf8 ustilago ma	206	35	56.5	326	2	Q8SK55_DUGDU	Q8sk55 dugong dugo
134	36	58.1	326	2	Q5CSP8_CRYPV	Q5csp8 cryptospori	207	35	56.5	326	2	Q3FGG5_9BURK	Q3fgg5 burkholderi
135	36	58.1	326	2	PLMN_BOVIN	P06868 bos taurus	208	35	56.5	326	2	Q458F4_9BURK	Q458f4 burkholderi
136	36	58.1	326	2	PLMN_RAT	Q01177 rattus norv	209	35	56.5	326	2	Q4LS05_9BURK	Q4ls05 burkholderi
137	36	58.1	326	2	Q5BKB6_RAT	Q5bkb6 rattus norv	210	35	56.5	326	2	Q392Z8_BURS3	Q392z8 burkholderi
138	36	58.1	326	2	Q3MDI7_ANAVT	Q3mdi7 anabaena va	211	35	56.5	326	2	Q5BEF3_ENEMI	Q5bef3 aspergillus
139	36	58.1	326	2	Q4IDT1_GIBZE	Q4idt1 gibberella	212	35	56.5	326	2	Q98RK2_MYCPU	Q98rk2 mycoplasma
140	36	58.1	326	2	MIPI_SCHPO	P87141 schizosacch	213	35	56.5	326	2	Q4S2M0_TETNG	Q4s2m0 tetraodon n
141	36	58.1	326	2	Q6BJ38_DEBHA	Q6bj38 debaryomyce	214	35	56.5	326	2	Q8Q7G8_9HIV1	Q8q7g8 human immun
142	36	58.1	326	2	Q48HQ4_PSELA	Q48hq4 pseudomonas	215	35	56.5	326	2	Q2QW32_ORYSA	Q2qw32 oryza sativ
143	36	58.1	326	2	Q9VAS8_DROME	Q9vas8 drosophila	216	35	56.5	326	2	Q4X086_ASPFU	Q4x086 aspergillus
144	36	58.1	326	2	Q4SSR8_TETNG	Q4ssr8 tetraodon n	217	35	56.5	326	2	Q4J680_AZOV1	Q4j680 azotobacter
145	36	58.1	326	2	Q28733_RABIT	Q28733 coryctolagus	218	35	56.5	326	2	Q5CM22_CRYHO	Q5cm22 cryptospori
146	35	56.5	100	1	YPTT_CLOBE	Q05627 clostridium	219	35	56.5	326	2	Q5CR38_CRYPV	Q5cr38 cryptospori
147	35	56.5	115	2	P72898_SYNY3	Q05627 synecocyst	220	35	56.5	326	2	Q817W7_DICDI	Q817w7 dictyosteli
148	35	56.5	127	2	Q9IUH0_9REOV	Q9iuho rotavirus a	221	35	56.5	326	2	Q5SE58_DICDI	Q5se58 dictyosteli
149	35	56.5	133	2	Q9IUU0_9REOV	Q9iuu0 rotavirus a	222	35	56.5	326	2	Q4V436_DROME	Q4v436 drosophila
150	35	56.5	133	2	Q9IUH6_9REOV	Q9iuh6 rotavirus a	223	34	54.8	326	2	Q9JZ49_NEIMB	Q9jz49 neisseria m
151	35	56.5	133	2	Q9IUH2_9REOV	Q9iuh2 rotavirus a	224	34	54.8	326	2	Q3N354_9DELT	Q3n354 syntrophoba
152	35	56.5	133	2	Q9IUH2_9REOV	Q9iuh2 rotavirus a	225	34	54.8	326	2	Q9YC57_AERPE	Q9yc57 aeropyrum p
153	35	56.5	136	2	Q7QQ51_GIALA	Q7qq51 giardia lam	226	34	54.8	326	2	Q73L26_TREDE	Q73l26 treponema d
154	35	56.5	141	2	Q3AHG5_SYNSC	Q3ahg5 synecococc	227	34	54.8	326	2	Q4Y285_PLACH	Q4y285 plasmodium
155	35	56.5	161	2	Q5TCM0_HUMAN	Q5tcml0 homo sapien	228	34	54.8	326	2	Q31PE3_SYNP7	Q31pe3 synecococc
156	35	56.5	186	2	Q3HMT7_9REOV	Q3hmt7 human rotav	229	34	54.8	326	2	Q6ZUJ9_HUMAN	Q6zuJ9 homo sapien
157	35	56.5	191	2	Q8S7E9_ORYSA	Q8s7e9 oryza sativ	230	34	54.8	326	2	Q5N4S7_SYNP6	Q5n4s7 synecococc
158	35	56.5	211	2	Q9SJ53_9RATH	Q9sj53 arabidopsis	231	34	54.8	326	2	Q9KXP7_STRCO	Q9kxp7 streptomyce
159	35	56.5	224	2	Q9SST3_9RATH	Q9sst3 arabidopsis	232	34	54.8	326	2	Q827S6_STRAW	Q827s6 streptomyce
160	35	56.5	224	2	Q4NFX0_9MICC	Q4nfx0 mastomys hi	233	34	54.8	326	2	Q2N6C9_9SPHN	Q2n6c9 erythrobact
161	35	56.5	229	2	Q6X2C2_MASHI	Q6x2c2 hylomyscus	234	34	54.8	326	2	Q72P03_LEPIC	Q72p03 leptospira
162	35	56.5	229	2	Q3FJW4_9BURK	Q3fjw4 burkholderi	235	34	54.8	326	2	Q8F7F6_LEPIC	Q8f7f6 leptospira
163	35	56.5	251	2	Q3J2F3_RHOPA	Q3j2f3 rhodospseudo	236	34	54.8	326	2	Q3N354_9DELT	Q3n354 syntrophoba
164	35	56.5	254	2	Q8QU08_9REOV	Q8qu08 human rotav	237	34	54.8	326	2	Q73L26_TREDE	Q73l26 treponema d
165	35	56.5	263	2	Q982T5_RHILO	Q982t5 rhizobium l	238	34	54.8	326	2	Q4Y285_PLACH	Q4y285 plasmodium
166	35	56.5	269	2	Q5DC23_SCHJA	Q5dc23 schistosoma	239	34	54.8	326	2	Q31PE3_SYNP7	Q31pe3 synecococc
167	35	56.5	270	2	Q9U231_CAEEL	Q9u231 caenorhabdi	240	34	54.8	326	2	Q6ZUJ9_HUMAN	Q6zuJ9 homo sapien
168	35	56.5	292	2	Q91C29_9REOV	Q91cz9 human rotav	241	34	54.8	326	2	Q5N4S7_SYNP6	Q5n4s7 synecococc
169	35	56.5	297	2	Q302Z4_STRSU	Q302z4 streptococc	242	34	54.8	326	2	Q9KXP7_STRCO	Q9kxp7 streptomyce
170	35	56.5	313	2	V509_ROTFG	P03365 porcine rot	243	34	54.8	326	2	Q827S6_STRAW	Q827s6 streptomyce
171	35	56.5	326	1	Q53AR6_9REOV	Q53ar6 human rotav	244	34	54.8	326	2	Q2N6C9_9SPHN	Q2n6c9 erythrobact
172	35	56.5	326	2	Q783Y3_9REOV	Q783y3 human rotav	245	34	54.8	326	2	Q72P03_LEPIC	Q72p03 leptospira
173	35	56.5	326	2	Q783Y4_9REOV	Q783y4 human rotav	246	34	54.8	326	2	Q8F7F6_LEPIC	Q8f7f6 leptospira
174	35	56.5	326	2	Q80BV1_9REOV	Q80bv1 human rotav	247	34	54.8	326	2	Q3N354_9DELT	Q3n354 syntrophoba
175	35	56.5	326	2	Q86231_9REOV	Q86231 rotavirus a	248	34	54.8	326	2	Q9YC57_AERPE	Q9yc57 aeropyrum p
176	35	56.5	326	2	Q8V281_9REOV	Q8v281 human rotav	249	34	54.8	326	2	Q73L26_TREDE	Q73l26 treponema d
177	35	56.5	326	2			250	34	54.8	326	2	Q4Y285_PLACH	Q4y285 plasmodium

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15	36	58.1	60	2	US-09-270-767-34098	Sequence 34098, A
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21	35	56.5	28	2	US-09-471-276-1203	Sequence 1203, Ap
22	35	56.5	277	2	US-09-134-000C-4158	Sequence 4158, Ap
23	35	56.5	326	1	US-07-603-133B-28	Sequence 28, Appl
24	35	56.5	358	2	US-09-252-991A-16785	Sequence 16785, A
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102	33	53.2	810	1	US-08-147-000B-29	Sequence 29, Appli	175	31	50.0	295	2	US-09-495-406-18	Sequence 18, Appl
103	33	53.2	810	2	US-09-086-514-1	Sequence 1, Appli	176	31	50.0	295	2	US-09-816-028A-32	Sequence 32, Appl
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111	33	53.2	1433	2	US-09-487-558B-60	Sequence 60, Appl	184	31	50.0	326	2	US-08-089-397A-13	Sequence 13, Appl
112	33	53.2	1455	2	US-08-840-062-5	Sequence 5, Appli	185	31	50.0	326	2	US-08-089-397A-14	Sequence 14, Appl
113	32	51.6	91	2	US-09-513-999C-6445	Sequence 6445, Ap	186	31	50.0	329	2	US-09-902-540-11951	Sequence 11951, A
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117	32	51.6	152	2	US-09-621-976-7670	Sequence 7670, Ap	190	31	50.0	390	2	US-09-949-016-9665	Sequence 9665, Ap
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122	32	51.6	259	2	US-09-270-767-38568	Sequence 38568, A	195	31	50.0	437	2	US-09-711-164-440	Sequence 440, App
123	32	51.6	259	2	US-09-270-767-53785	Sequence 53785, A	196	31	50.0	439	2	US-10-227-035-3	Sequence 3, Appli
124	32	51.6	324	2	US-09-252-991A-29070	Sequence 29070, A	197	31	50.0	441	2	US-09-949-016-10102	Sequence 10102, A
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130	32	51.6	569	2	US-09-252-991A-22870	Sequence 22870, A	203	31	50.0	494	2	US-09-949-016-10396	Sequence 10396, A
131	32	51.6	688	2	US-09-538-092-794	Sequence 794, App	204	31	50.0	502	1	US-08-481-337A-8	Sequence 8, Appli
132	32	51.6	975	2	US-10-094-749-2035	Sequence 2035, Ap	205	31	50.0	502	2	US-09-382-256-18	Sequence 18, Appl
133	32	51.6	979	1	US-08-308-881-6	Sequence 6, Appli	206	31	50.0	502	2	US-09-395-115-18	Sequence 18, Appl
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135	32	51.6	979	1	US-09-059-099-6	Sequence 6, Appli	208	31	50.0	502	2	US-08-334-179A-14	Sequence 14, Appl
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141	32	51.6	2343	2	US-09-324-867-2	Sequence 2, Appli	214	31	50.0	502	2	US-09-903-068C-18	Sequence 18, Appl
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143	31	50.0	64	2	US-09-248-796A-26024	Sequence 26024, A	216	31	50.0	502	5	PCT-US95-05467-8	Sequence 8, Appli
144	31	50.0	70	2	US-08-965-056-92	Sequence 92, Appl	217	31	50.0	633	2	US-09-489-039A-13729	Sequence 13729, A
145	31	50.0	74	2	US-09-774-639-115	Sequence 115, App	218	31	50.0	913	2	US-09-252-991A-29362	Sequence 29362, A
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149	31	50.0	104	2	US-09-513-999C-7814	Sequence 7814, Ap	222	31	50.0	1025	2	US-09-492-709A-283	Sequence 283, App
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151	31	50.0	133	2	US-09-134-000C-3923	Sequence 3923, Ap	224	31	50.0	1548	1	US-08-460-907B-7	Sequence 7, Appli
152	31	50.0	143	2	US-09-270-767-61267	Sequence 61267, A	225	31	50.0	1876	2	US-09-418-710-71	Sequence 71, Appl
153	31	50.0	146	2	US-09-270-767-40383	Sequence 40383, A	226	31	50.0	1876	2	US-09-839-479-70	Sequence 70, Appl
154	31	50.0	146	2	US-09-270-767-55599	Sequence 55599, A	227	30.5	49.2	622	2	US-09-605-703B-604	Sequence 604, App
155	31	50.0	178	2	US-09-540-236-2503	Sequence 2503, Ap	228	30.5	49.2	1218	2	US-09-605-703B-600	Sequence 600, App
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157	31	50.0	183	1	US-08-157-005-6	Sequence 6, Appli	230	30	48.4	25	2	US-09-440-772C-23	Sequence 23, Appl
158	31	50.0	183	1	US-08-799-464A-20	Sequence 20, Appl	231	30	48.4	25	2	US-09-440-772C-35	Sequence 35, Appl
159	31	50.0	183	2	US-08-747-863-6	Sequence 6, Appli	232	30	48.4	25	2	US-09-440-772C-40	Sequence 40, Appl
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161	31	50.0	183	2	US-09-019-793A-31	Sequence 31, Appl	234	30	48.4	32	2	US-09-625-972-30	Sequence 30, Appl
162	31	50.0	183	2	US-09-565-864-6	Sequence 6, Appli	235	30	48.4	33	2	US-09-433-428D-1	Sequence 1, Appli
163	31	50.0	183	2	US-08-301-435-77	Sequence 77, Appl	236	30	48.4	33	2	US-09-433-428D-20	Sequence 20, Appl
164	31	50.0	183	2	US-09-601-326-31	Sequence 31, Appl	237	30	48.4	37	2	US-08-817-441-86	Sequence 86, Appl
165	31	50.0	183	2	US-10-226-065-6	Sequence 6, Appli	238	30	48.4	40	2	US-08-894-699-41	Sequence 41, Appl
166	31	50.0	183	2	US-10-428-826-31	Sequence 31, Appl	239	30	48.4	40	2	US-09-444-410-41	Sequence 41, Appl
167	31	50.0	183	5	PCT-US95-09827-20	Sequence 20, Appl	240	30	48.4	42	2	US-09-284-819-1	Sequence 1, Appli
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- 4: /EMC Celerra_SID33/prodata/2/pubpaa/US10A_PUBCOMB.pgp:**
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- 6: /EMC Celerra_SID33/prodata/2/pubpaa/US11_PUBCOMB.pgp:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	13	US-10-797-626-1	Sequence 1, Appli
2	43	69.4	18	US-10-797-626-3	Sequence 3, Appli
3	43	69.4	19	US-10-797-626-2	Sequence 2, Appli
4	42	67.7	702	US-10-369-493-18088	Sequence 18088, A
5	39	62.9	145	US-10-424-599-149296	Sequence 149296,
6	39	62.9	333	US-10-135-8728-6	Sequence 6, Appli
7	39	62.9	466	US-10-753-164-2	Sequence 2, Appli
8	39	62.9	812	US-09-788-142-1	Sequence 1, Appli
9	39	62.9	812	US-09-761-120-1	Sequence 1, Appli
10	39	62.9	812	US-09-873-676-81	Sequence 81, Appli
11	39	62.9	812	US-09-335-325-1	Sequence 1, Appli
12	39	62.9	812	US-10-131-241-1	Sequence 1, Appli
13	39	62.9	812	US-10-127-066-1	Sequence 1, Appli
14	39	62.9	812	US-10-402-364-1	Sequence 1, Appli
15	39	62.9	812	US-10-401-108-1	Sequence 1, Appli
16	39	62.9	812	US-11-010-874-1	Sequence 1, Appli
17	39	62.9	812	US-11-108-459-6	Sequence 6, Appli
18	38	61.3	107	US-10-264-237-2106	Sequence 2106, Ap
19	38	61.3	207	US-10-767-701-36927	Sequence 36927, A
20	37	59.7	52	US-10-437-963-149804	Sequence 149804,
21	37	59.7	190	US-10-767-701-41842	Sequence 41842, A
22	37	59.7	292	US-09-996-194-20	Sequence 20, Appli
23	37	59.7	292	US-10-164-966-37	Sequence 37, Appli
24	37	59.7	292	US-11-245-400-37	Sequence 37, Appli
25	37	59.7	407	US-10-425-115-285007	Sequence 285007,
26	37	59.7	412	US-10-425-114-38228	Sequence 38228, A
27	37	59.7	412	US-10-425-114-59595	Sequence 59595, A

28	37	59.7	460	6	US-11-087-099-2946	Sequence 2946, Ap
29	37	59.7	460	6	US-11-188-298-13823	Sequence 13823, A
30	36	58.1	18	3	US-09-864-761-36257	Sequence 36257, A
31	36	58.1	66	4	US-10-437-963-131021	Sequence 131021,
32	36	58.1	215	4	US-10-425-115-205311	Sequence 205311,
33	36	58.1	252	4	US-10-369-493-3516	Sequence 3516, Ap
34	36	58.1	252	4	US-10-437-963-110876	Sequence 110876,
35	36	58.1	288	4	US-10-616-897-3	Sequence 3, Appli
36	36	58.1	375	4	US-10-282-122A-53921	Sequence 53921, A
37	36	58.1	560	4	US-10-616-897-11	Sequence 11, Appli
38	36	58.1	704	4	US-10-437-963-178458	Sequence 178458
39	36	58.1	812	3	US-09-825-751A-71	Sequence 71, Appli
40	36	58.1	812	5	US-10-851-438-71	Sequence 71, Appli
41	36	58.1	1239	4	US-10-425-115-214664	Sequence 214664,
42	36	58.1	1313	4	US-10-437-421-22	Sequence 22, Appli
43	36	58.1	2015	6	US-11-097-143-24462	Sequence 24462, A
44	35	56.5	28	5	US-10-926-683-1203	Sequence 1203, Ap
45	35	56.5	59	4	US-10-424-599-154063	Sequence 154063,
46	35	56.5	77	4	US-10-437-963-199030	Sequence 199030,
47	35	56.5	96	4	US-10-425-115-201385	Sequence 201385,
48	35	56.5	360	5	US-10-450-763-52571	Sequence 52571, A
49	35	56.5	393	5	US-10-722-045-7	Sequence 7, Appli
50	35	56.5	393	5	US-10-466-811-6	Sequence 6, Appli
51	35	56.5	403	3	US-09-815-242-10574	Sequence 10574, A
52	35	56.5	403	4	US-10-282-122A-42574	Sequence 42574, A
53	35	56.5	404	3	US-09-815-242-4923	Sequence 4923, Ap
54	35	56.5	504	4	US-10-437-963-182249	Sequence 182249,
55	35	56.5	535	4	US-10-425-115-214521	Sequence 214521,
56	35	56.5	629	5	US-10-450-763-48138	Sequence 48138, A
57	35	56.5	664	4	US-10-282-122A-62708	Sequence 62708, A
58	35	56.5	667	5	US-10-450-763-59096	Sequence 59096, A
59	35	56.5	902	4	US-10-437-963-117835	Sequence 117835,
60	35	56.5	2964	5	US-10-732-923-13552	Sequence 13552, A
61	34	54.8	67	4	US-10-425-115-246349	Sequence 246349,
62	34	54.8	20	5	US-10-311-827-16	Sequence 16, Appli
63	34	54.8	45	5	US-10-311-827-22	Sequence 22, Appli
64	34	54.8	47	5	US-10-916-827-23	Sequence 23, Appli
65	34	54.8	54	4	US-10-437-963-196236	Sequence 196236,
66	34	54.8	61	4	US-10-437-963-147188	Sequence 147188,
67	34	54.8	64	3	US-09-867-550-1096	Sequence 1096, Ap
68	34	54.8	74	4	US-10-424-599-226553	Sequence 226553,
69	34	54.8	81	4	US-10-424-599-248178	Sequence 248178,
70	34	54.8	85	4	US-10-425-115-203172	Sequence 203172,
71	34	54.8	96	4	US-10-424-599-226555	Sequence 226555,
72	34	54.8	96	4	US-10-425-115-338461	Sequence 338461,
73	34	54.8	126	4	US-10-424-599-279936	Sequence 279936,
74	34	54.8	130	4	US-10-424-599-210126	Sequence 210126,
75	34	54.8	131	4	US-10-425-115-221903	Sequence 221903,
76	34	54.8	145	4	US-10-425-115-293341	Sequence 293341,
77	34	54.8	151	4	US-10-156-761-14376	Sequence 14376, A
78	34	54.8	179	4	US-10-282-122A-73351	Sequence 73351, A
79	34	54.8	179	4	US-10-282-122A-75411	Sequence 75411, A
80	34	54.8	192	4	US-10-424-599-282928	Sequence 282928,
81	34	54.8	192	4	US-10-767-701-40433	Sequence 40433, A
82	34	54.8	208	4	US-10-437-963-175540	Sequence 175540,
83	34	54.8	211	3	US-09-764-864-1582	Sequence 1582, Ap
84	34	54.8	217	4	US-10-424-599-180981	Sequence 180981,
85	34	54.8	245	4	US-10-369-493-4972	Sequence 4972, Ap
86	34	54.8	262	4	US-10-282-122A-60891	Sequence 60891, A
87	34	54.8	262	6	US-11-045-004-1626	Sequence 1626, Ap
88	34	54.8	276	4	US-10-424-599-276227	Sequence 276227,
89	34	54.8	278	4	US-10-282-122A-53119	Sequence 53119, A
90	34	54.8	303	6	US-11-097-143-32523	Sequence 32523, A
91	34	54.8	304	4	US-10-425-114-70322	Sequence 70322, A
92	34	54.8	323	4	US-10-312-352-17	Sequence 17, Appli
93	34	54.8	326	4	US-10-291-265-382	Sequence 382, App
94	34	54.8	326	5	US-10-291-265-854	Sequence 854, App
95	34	54.8	326	5	US-10-311-827-14	Sequence 14, Appli
96	34	54.8	326	6	US-11-000-463-382	Sequence 382, App
97	34	54.8	326	6	US-11-000-463-884	Sequence 884, App
98	34	54.8	335	4	US-10-363-829-444	Sequence 444, App
99	34	54.8	340	6	US-11-097-143-13917	Sequence 13917, A
100	34	54.8	370	4	US-10-425-114-45808	Sequence 45808, A

101	34	54.8	374	5	US-10-732-923-12108	Sequence 12108, A	174	33	53.2	126	4	US-10-424-599-152631	Sequence 152631,
102	34	54.8	374	6	US-11-087-099-2515	Sequence 2515, Ap	175	33	53.2	128	5	US-10-450-763-54480	Sequence 54480, A
103	34	54.8	388	4	US-10-240-535-2	Sequence 2, Appli	176	33	53.2	133	3	US-09-852-976-2	Sequence 2, Appli
104	34	54.8	388	4	US-10-389-301-4	Sequence 4, Appli	177	33	53.2	133	3	US-10-424-599-151881	Sequence 151881,
105	34	54.8	388	4	US-10-388-931-8	Sequence 4, Appli	178	33	53.2	136	4	US-10-741-601-410	Sequence 410, App
106	34	54.8	388	4	US-10-351-161A-8	Sequence 8, Appli	179	33	53.2	136	5	US-10-995-561-760	Sequence 760, App
107	34	54.8	388	5	US-10-311-827-4	Sequence 4, Appli	180	33	53.2	142	3	US-09-738-626-4438	Sequence 4438, Ap
108	34	54.8	406	4	US-10-424-599-237922	Sequence 237922,	181	33	53.2	142	5	US-10-494-672-362	Sequence 362, App
109	34	54.8	432	4	US-10-424-599-209041	Sequence 209041,	182	33	53.2	148	4	US-10-424-599-208070	Sequence 208070,
110	34	54.8	452	4	US-10-032-585-7906	Sequence 7906, Ap	183	33	53.2	149	4	US-10-741-601-412	Sequence 412, App
111	34	54.8	468	5	US-10-626-832-19	Sequence 19, Appl	184	33	53.2	149	5	US-10-995-561-763	Sequence 763, App
112	34	54.8	473	4	US-10-437-963-193704	Sequence 193704,	185	33	53.2	150	4	US-10-424-599-179372	Sequence 179372,
113	34	54.8	477	4	US-10-425-114-50068	Sequence 50068, A	186	33	53.2	152	4	US-10-425-115-323941	Sequence 323941,
114	34	54.8	481	4	US-10-087-192-123	Sequence 123, App	187	33	53.2	154	4	US-10-424-599-225499	Sequence 225499,
115	34	54.8	483	4	US-10-732-923-222303	Sequence 22303, A	188	33	53.2	154	4	US-10-437-963-183228	Sequence 183228,
116	34	54.8	497	4	US-10-425-114-46737	Sequence 46737, A	189	33	53.2	159	4	US-10-424-599-260375	Sequence 260375,
117	34	54.8	497	4	US-10-425-115-358371	Sequence 358371,	190	33	53.2	159	4	US-10-767-701-38997	Sequence 38997, A
118	34	54.8	512	4	US-10-425-114-52038	Sequence 52038, A	191	33	53.2	164	4	US-10-156-761-11069	Sequence 11069, A
119	34	54.8	525	4	US-10-424-599-215406	Sequence 215406,	192	33	53.2	164	6	US-11-166-412-225	Sequence 412, 225
120	34	54.8	525	5	US-10-732-923-222301	Sequence 22301, A	193	33	53.2	172	5	US-10-467-657-4514	Sequence 4514, Ap
121	34	54.8	529	4	US-10-425-115-351332	Sequence 351332,	194	33	53.2	180	4	US-10-425-115-326102	Sequence 326102,
122	34	54.8	529	4	US-10-425-115-351337	Sequence 351337,	195	33	53.2	186	4	US-10-104-047-2146	Sequence 2146, Ap
123	34	54.8	531	4	US-10-424-599-229987	Sequence 229987,	196	33	53.2	186	6	US-11-072-512-2146	Sequence 2146, Ap
124	34	54.8	531	5	US-10-732-923-222307	Sequence 22307, A	197	33	53.2	197	4	US-10-424-599-152633	Sequence 152633,
125	34	54.8	531	5	US-10-732-923-222309	Sequence 22309, A	198	33	53.2	205	4	US-10-408-765A-2918	Sequence 2918, Ap
126	34	54.8	532	5	US-10-732-923-22232	Sequence 22252, A	199	33	53.2	213	4	US-10-023-386-3754	Sequence 3754, A
127	34	54.8	532	5	US-10-732-923-222310	Sequence 22310, A	200	33	53.2	216	4	US-10-425-115-331680	Sequence 331680,
128	34	54.8	532	5	US-10-732-923-222312	Sequence 22312, A	201	33	53.2	228	3	US-09-939-537-27	Sequence 27, Appl
129	34	54.8	533	4	US-10-310-154-699	Sequence 699, App	202	33	53.2	228	3	US-09-243-008-27	Sequence 27, Appl
130	34	54.8	533	5	US-10-732-923-611	Sequence 611, App	203	33	53.2	228	4	US-10-079-130-4	Sequence 4, Appli
131	34	54.8	534	4	US-10-425-115-358372	Sequence 358372,	204	33	53.2	244	4	US-10-616-897-15	Sequence 15, Appl
132	34	54.8	539	4	US-10-425-114-54996	Sequence 54996, A	205	33	53.2	244	4	US-10-616-897-17	Sequence 17, Appl
133	34	54.8	539	4	US-10-425-114-56043	Sequence 56043, A	206	33	53.2	261	4	US-10-369-493-18303	Sequence 18303, A
134	34	54.8	539	5	US-10-732-923-222308	Sequence 22308, A	207	33	53.2	277	4	US-10-267-502-332	Sequence 332, App
135	34	54.8	540	4	US-10-424-599-276231	Sequence 276231,	208	33	53.2	277	6	US-11-097-143-24675	Sequence 24675, A
136	34	54.8	543	5	US-10-732-923-222300	Sequence 22300, A	209	33	53.2	283	4	US-10-616-897-1	Sequence 1, Appli
137	34	54.8	624	4	US-10-032-585-7797	Sequence 7797, Ap	210	33	53.2	286	4	US-10-616-897-4	Sequence 4, Appli
138	34	54.8	658	4	US-10-425-114-63115	Sequence 63115, A	211	33	53.2	288	4	US-10-616-897-2	Sequence 2, Appli
139	34	54.8	693	5	US-10-714-995-24	Sequence 24, Appl	212	33	53.2	297	6	US-11-097-143-31473	Sequence 31473, A
140	34	54.8	693	6	US-11-097-143-10674	Sequence 10674, A	213	33	53.2	310	6	US-11-166-412-224	Sequence 224, App
141	34	54.8	849	5	US-10-450-763-59554	Sequence 59554, A	214	33	53.2	326	3	US-09-284-320-88	Sequence 88, Appl
142	34	54.8	994	5	US-10-450-763-56037	Sequence 56037, A	215	33	53.2	346	3	US-09-808-701A-32	Sequence 32, Appl
143	34	54.8	1022	4	US-10-437-963-127708	Sequence 127708,	216	33	53.2	346	4	US-10-233-131-32	Sequence 32, Appl
144	34	54.8	1033	4	US-10-425-115-343179	Sequence 343179,	217	33	53.2	346	4	US-10-240-145-84	Sequence 84, Appl
145	34	54.8	1079	4	US-10-425-115-205898	Sequence 205898,	218	33	53.2	346	5	US-10-291-128-84	Sequence 84, Appl
146	34	54.8	1145	4	US-10-425-114-70456	Sequence 70456, A	219	33	53.2	354	6	US-11-188-298-15654	Sequence 15654, A
147	34	54.8	1184	5	US-10-450-763-51085	Sequence 51085, A	220	33	53.2	355	6	US-11-166-412-223	Sequence 223, App
148	34	54.8	1266	6	US-11-097-143-32124	Sequence 32124, A	221	33	53.2	363	6	US-11-188-298-13217	Sequence 13217, A
149	34	54.8	1456	3	US-09-870-759-95	Sequence 95, Appl	222	33	53.2	374	3	US-09-798-584-1	Sequence 1, Appli
150	34	54.8	1456	3	US-09-751-708A-95	Sequence 95, Appl	223	33	53.2	374	4	US-10-146-733-41	Sequence 41, Appl
151	34	54.8	1456	4	US-10-255-027-1217	Sequence 1217, Ap	224	33	53.2	374	4	US-10-257-022-6	Sequence 6, Appli
152	34	54.8	1456	4	US-10-428-817A-91	Sequence 91, Appl	225	33	53.2	374	4	US-10-074-978A-194	Sequence 194, App
153	34	54.8	1456	5	US-10-723-860-673	Sequence 673, App	226	33	53.2	378	4	US-10-437-963-194391	Sequence 194391,
154	34	54.8	1456	5	US-10-937-758A-72	Sequence 72, Appl	227	33	53.2	382	4	US-10-425-114-37688	Sequence 37688, A
155	33	53.2	29	3	US-09-933-767-281	Sequence 281, App	228	33	53.2	387	4	US-10-767-701-45657	Sequence 45657, A
156	33	53.2	29	4	US-10-004-860-281	Sequence 281, App	229	33	53.2	388	6	US-11-096-568A-21682	Sequence 21682, A
157	33	53.2	29	4	US-10-023-282-281	Sequence 281, App	230	33	53.2	394	4	US-10-437-963-177158	Sequence 177158,
158	33	53.2	44	4	US-09-864-761-36103	Sequence 36103, A	231	33	53.2	395	4	US-10-437-963-177156	Sequence 177156,
159	33	53.2	48	4	US-10-425-115-196785	Sequence 196785,	232	33	53.2	412	6	US-11-087-099-10691	Sequence 10691, A
160	33	53.2	55	4	US-10-437-963-133206	Sequence 133206,	233	33	53.2	416	4	US-10-282-122A-72263	Sequence 72263, A
161	33	53.2	68	4	US-10-424-599-152676	Sequence 152676,	234	33	53.2	421	4	US-10-282-122A-70083	Sequence 70083, A
162	33	53.2	71	3	US-09-933-767-355	Sequence 355, App	235	33	53.2	427	3	US-09-847-208-5	Sequence 5, Appli
163	33	53.2	71	4	US-10-004-860-355	Sequence 355, App	236	33	53.2	427	4	US-10-000-439-5	Sequence 5, Appli
164	33	53.2	71	4	US-10-023-282-355	Sequence 355, App	237	33	53.2	428	3	US-09-916-230-1	Sequence 1, Appli
165	33	53.2	74	6	US-11-188-298-7364	Sequence 7364, A	238	33	53.2	428	3	US-09-949-375A-1	Sequence 1, Appli
166	33	53.2	84	4	US-10-425-115-287801	Sequence 287801,	239	33	53.2	428	4	US-10-047-542-60	Sequence 60, Appl
167	33	53.2	86	4	US-10-424-599-268163	Sequence 268163,	240	33	53.2	428	4	US-10-363-954A-1	Sequence 1, Appli
168	33	53.2	86	4	US-10-767-701-56155	Sequence 56155, A	241	33	53.2	428	5	US-10-493-909-60	Sequence 60, Appl
169	33	53.2	99	5	US-10-450-763-54479	Sequence 54479, A	242	33	53.2	441	3	US-09-949-375A-7	Sequence 7, Appli
170	33	53.2	105	6	US-11-075-351-55	Sequence 55, Appl	243	33	53.2	441	5	US-10-732-923-22261	Sequence 22261, A
171	33	53.2	107	4	US-10-425-115-223798	Sequence 223798,	244	33	53.2	446	5	US-10-732-923-22261	Sequence 22261, A
172	33	53.2	110	4	US-10-425-114-49667	Sequence 49667, A	245	33	53.2	456	5	US-10-756-149-5775	Sequence 5775, Ap
173	33	53.2	125	4	US-10-425-115-349493	Sequence 349493,	246	33	53.2	457	4	US-10-424-599-208072	Sequence 208072,

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:11:07 ; Search time 140.98 Seconds
(without alignments)
61.619 Million cell updates/sec

Title: US-10-797-626-2

Perfect score: 94
Sequence: 1 KGCSTONQALLSLIVGKA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	100.0	19	ADS18078	Ads18078 Laminin s
2	74.5	79.3	18	ADS18079	Ads18079 Laminin s
3	45	47.9	324	ABO80324	ABO80324 Pseudomon
4	45	47.9	371	ABO81209	ABO81209 Pseudomon
5	44	46.8	865	AAG78665	AAG78665 Moritella
6	43	45.7	13	ADS18077	Ads18077 Laminin s
7	43	45.7	139	Aau33241	Aau33241 Novel hum
8	43	45.7	235	ABU34024	ABU34024 Protein e
9	43	45.7	337	ABU00184	ABU00184 Human nov
10	43	45.7	449	ABU71938	ABU71938 Drosophil
11	43	45.7	449	Aau74634	Aau74634 Oestrogen
12	43	45.7	452	ABU10110	ABU10110 Mouse cas
13	43	45.7	452	ADB79812	ADB79812 Rat caapa
14	43	45.7	452	ADE63000	ADE63000 Rat Prote
15	43	45.7	621	ADQ67726	ADQ67726 Novel hum
16	43	45.7	751	ABG69453	ABG69453 Human nov
17	43	45.7	751	ABU60658	ABU60658 Human kin
18	43	45.7	751	ADH62285	ADH62285 Novel hum
19	43	45.7	751	AEE28231	AEE28231 Human kin
20	43	45.7	764	ABG69452	ABG69452 Human nov
21	43	45.7	764	ABU60657	ABU60657 Human kin
22	43	45.7	764	ADH62283	ADH62283 Novel hum
23	43	45.7	764	AEE28229	AEE28229 Human kin

24	43	45.7	776	5	ABG69461	Abg69461 Human nov
25	43	45.7	776	6	ABU60666	Abu60666 Human kin
26	43	45.7	776	8	ADH62301	Adh62301 Novel hum
27	43	45.7	776	10	AEE28247	Aee28247 Human kin
28	43	45.7	789	5	ABG69460	Abg69460 Human nov
29	43	45.7	789	6	ABU60665	Abu60665 Human kin
30	43	45.7	789	8	ADH62299	Adh62299 Novel hum
31	43	45.7	789	10	AEE28245	Aee28245 Human kin
32	43	45.7	838	5	ABG69469	Abg69469 Human nov
33	43	45.7	838	6	ABU60674	Abu60674 Human kin
34	43	45.7	838	8	ADH62317	Adh62317 Novel hum
35	43	45.7	838	10	AEE28263	Aee28263 Human kin
36	43	45.7	851	5	ABG69468	Abg69468 Human nov
37	43	45.7	851	6	ABU60673	Abu60673 Human kin
38	43	45.7	851	8	ADH62315	Adh62315 Novel hum
39	43	45.7	851	10	AEE28261	Aee28261 Human kin
40	43	45.7	863	5	ABG69465	Abg69465 Human nov
41	43	45.7	863	6	ABU60670	Abu60670 Human kin
42	43	45.7	863	8	ADH62309	Adh62309 Novel hum
43	43	45.7	863	10	AEE28255	Aee28255 Human kin
44	43	45.7	864	5	ABG69451	Abg69451 Human nov
45	43	45.7	864	6	ABU60656	Abu60656 Human kin
46	43	45.7	864	8	ADH62281	Adh62281 Novel hum
47	43	45.7	864	10	AEE28227	Aee28227 Human kin
48	43	45.7	870	5	ABG69450	Abg69450 Human nov
49	43	45.7	870	6	ABU60655	Abu60655 Human kin
50	43	45.7	870	8	ADH62279	Adh62279 Novel hum
51	43	45.7	870	10	AEE28225	Aee28225 Human kin
52	43	45.7	876	5	ABG69464	Abg69464 Human nov
53	43	45.7	876	6	ABU60669	Abu60669 Human kin
54	43	45.7	876	8	ADH62307	Adh62307 Novel hum
55	43	45.7	876	10	AEE28253	Aee28253 Human kin
56	43	45.7	889	5	ABG69459	Abg69459 Human nov
57	43	45.7	889	6	ABU60664	Abu60664 Human kin
58	43	45.7	889	8	ADH62297	Adh62297 Novel hum
59	43	45.7	889	10	AEE28243	Aee28243 Human kin
60	43	45.7	895	5	ABG69458	Abg69458 Human nov
61	43	45.7	895	6	ABU60663	Abu60663 Human kin
62	43	45.7	895	8	ADH62295	Adh62295 Novel hum
63	43	45.7	895	10	AEE28241	Aee28241 Human kin
64	43	45.7	951	5	ABG69467	Abg69467 Human nov
65	43	45.7	951	6	ABU60672	Abu60672 Human kin
66	43	45.7	951	8	ADH62313	Adh62313 Novel hum
67	43	45.7	951	10	AEE28259	Aee28259 Human kin
68	43	45.7	957	5	ABG69466	Abg69466 Human nov
69	43	45.7	957	6	ABU60671	Abu60671 Human kin
70	43	45.7	957	8	ADH62311	Adh62311 Novel hum
71	43	45.7	957	10	AEE28257	Aee28257 Human kin
72	43	45.7	976	5	ABG69463	Abg69463 Human nov
73	43	45.7	976	6	ABU60668	Abu60668 Human kin
74	43	45.7	976	8	ADH62305	Adh62305 Novel hum
75	43	45.7	976	10	AEE28251	Aee28251 Human kin
76	43	45.7	982	5	ABG69462	Abg69462 Human nov
77	43	45.7	982	6	ABU60667	Abu60667 Human kin
78	43	45.7	982	8	ADH62303	Adh62303 Novel hum
79	43	45.7	982	10	AEE28249	Aee28249 Human kin
80	43	45.7	1270	7	ADJ70447	Adj70447 Human hea
81	43	45.7	1270	9	AEA52444	Aea52444 Human tau
82	43	45.7	1308	6	ABR57072	AbR57072 Human tau
83	43	45.7	1308	9	ADV97846	Adv97846 Murine pr
84	43	45.7	1321	8	ADN07671	Adn07671 Human bra
85	43	45.7	1331	7	ADC10010	Adc10010 Human NOV
86	42	44.7	313	4	ABG09606	Abg09606 Novel hum
87	42	44.7	330	4	ABG02784	Abg02784 Novel hum
88	42	44.7	719	2	AAR25069	Aar25069 mLI-F-R. 3
89	42	44.7	719	2	AAR45775	Aar45775 Murine le
90	42	44.7	719	2	AAR49507	Aar49507 Human LIF
91	42	44.7	719	2	AAR74096	Aar74096 Murine le
92	42	44.7	1092	8	ABO84694	ABO84694 Mouse can
93	41	43.6	122	7	ADF59526	Adf59526 Human pol
94	41	43.6	154	4	ABG223905	Abg223905 Novel hum
95	41	43.6	167	7	ADM25939	Adm25939 Hyperther
96	41	43.6	263	8	ADT89334	Adt89334 Mouse onc

97	41	43.6	263	9	AED01095	Aed01095 Mouse onc	170	39	41.5	376	3	AA55841	Aay55841 Human cyt
98	41	43.6	421	4	ABB63148	Abb63148 Drosophil	171	39	41.5	376	7	ADD14094	Add14094 Human Pro
99	41	43.6	428	4	ABB60476	Abb60476 Drosophil	172	39	41.5	376	7	AD59314	Ad59314 Human Pro
100	41	43.6	431	4	ABG15132	Abg15132 Novel hum	173	39	41.5	376	8	ADF76331	Adf76331 Novel hum
101	41	43.6	476	7	ADF28933	Adf28933 Sheep ang	174	39	41.5	376	8	ADI53096	Adi53096 Human gra
102	41	43.6	1154	6	ADAI3344	Adai3344 Human int	175	39	41.5	376	8	ADL83201	Adl83201 Human PRO
103	41	43.6	1401	8	ADLI3306	Adli3306 Human ste	176	39	41.5	376	8	ADP24324	Adp24324 PRO poly
104	41	43.6	1401	9	ADX07508	Adx07508 Cyclin-de	177	39	41.5	376	8	ADT98544	Adt98544 Human ser
105	41	43.6	1634	2	AAR42452	Aar42452 Enzyme in	178	39	41.5	376	8	ADT98544	Adt98544 Human ser
106	41	43.6	1642	2	AAR89400	Aar89400 S. putref	179	39	41.5	398	5	ABP30071	Abp30071 Streptoco
107	41	43.6	2756	2	AAR99462	Aar99462 Biosynthe	180	39	41.5	398	8	ADV88303	Adv88303 Streptoco
108	41	43.6	2756	3	AAW37050	Aaw37050 S. putref	181	39	41.5	398	8	ADV9556	Adv9556 Streptoco
109	41	43.6	2756	3	AAAB10467	Aab10467 Shewanell	182	39	41.5	398	8	ADV81725	Adv81725 Streptoco
110	41	43.6	2756	4	AAG64455	Aag64455 S. putref	183	39	41.5	398	6	ABU39183	Abu39183 Protein e
111	40.5	43.1	254	6	ABU33391	Abu33391 Protein e	184	39	41.5	400	6	ADT49283	Adt49283 Pectate i
112	40.5	43.1	254	9	ABE39665	Aeb39665 L. pneumo	185	39	41.5	466	8	ADO71642	Ado71642 Pseudomon
113	40.5	43.1	261	9	ABE36245	Aeb36245 L. pneumo	186	39	41.5	485	7	ABO71642	Ab071642 Pseudomon
114	40.5	43.1	332	4	AAAB76570	Aab76570 Corynebac	187	39	41.5	529	9	AED26464	Aed26464 Novel hum
115	40.5	43.1	332	4	AAG92306	Aag92306 C. glutami	188	39	41.5	530	4	ADG27693	Adg27693 Human nov
116	40.5	43.1	587	4	AAB49986	Aab49986 P. gallin	189	39	41.5	566	4	AAU30834	Aau30834 Novel hum
117	40	42.6	115	4	AAU45567	Aau45567 Propionib	190	39	41.5	582	4	ABB63987	Abb63987 Drosophil
118	40	42.6	115	6	ABM42086	Abm42086 Propionib	191	39	41.5	826	3	AA595050	Aay95050 Candida a
119	40	42.6	142	3	AAG57167	Aag57167 Arabidops	192	39	41.5	1049	8	ADN18867	Adn18867 Bacterial
120	40	42.6	192	4	AAU46473	Aau46473 Propionib	193	39	41.5	1184	4	ABG20726	Abg20726 Novel hum
121	40	42.6	192	6	ABM42992	Abm42992 Propionib	194	39	41.5	1184	4	ADA89491	Ada89491 Staphyloc
122	40	42.6	209	5	ABP26506	Abp26506 Streptoco	195	39	41.5	1450	6	AAU24033	Aar24033 Soluble m
123	40	42.6	248	8	ADL05903	Adl05903 M. catarr	196	39	41.5	1456	6	ABU79121	Abu79121 Anglostet
124	40	42.6	255	8	ADX95159	Adx95159 Plant ful	197	39	41.5	1456	7	ADF43375	Adf43375 Mannose r
125	40	42.6	278	6	ABU25195	Abu25195 Protein e	198	39	41.5	1456	7	ADN39899	Adn39899 Cancer/an
126	40	42.6	292	8	ADX67591	Adx67591 Plant ful	199	39	41.5	1456	7	ADN95147	Adn95147 Human BBC
127	40	42.6	431	4	AAB79671	Aab79671 Corynebac	200	39	41.5	1456	8	ADN12439	Adn12439 Human ste
128	40	42.6	436	8	ADM98815	Adm98815 HMG-CoA r	201	39	41.5	1456	8	ADQ17856	Adq17856 Human sof
129	40	42.6	436	8	ADS42948	Ads42948 Bacterial	202	39	41.5	1456	8	ADP23714	Adp23714 PRO poly
130	40	42.6	477	8	ADX87538	Adx87538 Plant ful	203	39	41.5	1456	9	AEA03046	Aea03046 Glycophor
131	40	42.6	563	7	ABO70641	Ab070641 Pseudomon	204	39	41.5	1456	9	AAU34072	Aau34072 Staphyloc
132	40	42.6	617	8	ADN24090	Adn24090 Bacterial	205	39	41.5	1491	6	ABU16457	Abu16457 Protein e
133	40	42.6	645	4	AAG82945	Aag82945 S. epider	206	39	41.5	1499	6	AAU36569	Aau36569 Staphyloc
134	40	42.6	933	6	ABU43104	Abu43104 Protein e	207	39	41.5	1502	6	ABM71608	Abm71608 Bacterial
135	40	42.6	1501	4	AAG82878	Aag82878 S. epider	208	39	41.5	2335	8	ADN15908	Adn15908 Bacterial
136	40	42.6	1509	6	ABU43942	Abu43942 Protein e	209	39	41.5	18	ADR42896	Adr42896 Denatured	
137	40	42.6	1510	2	AAU01312	Aay01312 Glutamine	210	38.5	41.0	350	8	AAU87117	Aau87117 Novel cen
138	40	42.6	1510	4	AAB79669	Aab79669 Corynebac	211	38.5	41.0	350	8	ADI54432	Adi54432 Murine pa
139	40	42.6	1510	4	AAG89953	Aag89953 C. glutami	212	38.5	41.0	783	3	ABM23648	Abm23648 Murine pa
140	40	42.6	1510	7	ADDI13595	Adi13595 C. glutami	213	38.5	41.0	1006	2	AAW77290	Aaw77290 Human dif
141	40	42.6	1529	5	ABP39100	Abp39100 Staphyloc	214	38.5	41.0	1006	2	AAW77290	Aaw77290 Human dif
142	40	42.6	1529	8	ADSO7312	Adso7312 Staphyloc	215	38.5	41.0	1006	2	AAW77290	Aaw77290 Human dif
143	39.5	42.0	203	4	ABO36735	Ab036735 Putative	216	38	40.4	18	ADH16067	Adh16067 Gliadin r	
144	39.5	42.0	333	6	ABU39107	Abu39107 Protein e	217	38	40.4	18	ADH15337	Adh15337 Gliadin r	
145	39.5	42.0	652	7	ABM88164	Abm88164 Rice abio	218	38	40.4	70	3	AAH40912	Aah40912 Human ORF
146	39.5	42.0	843	9	ABE13424	Aeb13424 Human pro	219	38	40.4	79	5	ABP08060	Abp08060 Human ORF
147	39.5	42.0	885	9	ABE13426	Aeb13426 Human pro	220	38	40.4	79	9	ADM69713	Adm69713 D melanog
148	39.5	42.0	898	4	ABG15488	Abg15488 Novel hum	221	38	40.4	91	10	ABE60259	Aee60259 Cat chlam
149	39.5	42.0	933	8	ADT77664	Adt77664 Splice va	222	38	40.4	192	2	AAU32780	Aay32780 HIV chemo
150	39.5	42.0	1604	4	AAAB47327	Aab47327 FCRR4. 8/	223	38	40.4	192	5	ABP00179	Abp00179 Human ORF
151	39.5	42.0	2015	4	ABE65890	Ab65890 Drosophil	224	38	40.4	224	3	AAU20878	Aag20878 Arabidops
152	39	41.5	2015	4	ABE65890	Ab65890 Mucant pe	225	38	40.4	224	3	AAU20878	Aag20878 Arabidops
153	39	41.5	87	3	AAAB94999	Aam94999 Human rep	226	38	40.4	244	7	ABO68854	Ab068854 Pseudomon
154	39	41.5	87	4	ABE95707	Ab95707 Human tes	227	38	40.4	244	7	ADC00171	Adc00171 Enteroha
155	39	41.5	156	8	ADO07062	Ado07062 Human pro	228	38	40.4	263	3	AAU50880	Aag50880 Arabidops
156	39	41.5	227	6	ABU38639	Abu38639 Protein e	229	38	40.4	263	3	AAU50880	Aag50880 Arabidops
157	39	41.5	238	5	ABP26194	Abp26194 Streptoco	230	38	40.4	324	7	ADL98001	Adl98001 Human olf
158	39	41.5	250	9	AED01099	Aed01099 Rat oncos	231	38	40.4	329	6	ABU43856	Abu43856 Protein e
159	39	41.5	269	6	ABU19123	Abu19123 Protein e	232	38	40.4	333	6	ABM67449	Abm67449 Photorhab
160	39	41.5	273	8	ADP24567	Adp24567 PRO poly	233	38	40.4	337	4	AAU79806	Aam79806 Human pro
161	39	41.5	297	7	ADH86302	Adh86302 Enterococ	234	38	40.4	337	4	AAU79806	Aam79806 Human pro
162	39	41.5	309	7	ABM85441	Abm85441 Human pro	235	38	40.4	357	6	ABU49081	Abu49081 Protein e
163	39	41.5	322	8	ADO07060	Ado07060 Human pro	236	38	40.4	369	5	ABP74089	Abp74089 Candida a
164	39	41.5	328	8	ABM82806	Abm82806 Human dia	237	38	40.4	381	4	AAQ17874	Aaq17874 C. glutami
165	39	41.5	328	8	ABM82805	Abm82805 Human dia	238	38	40.4	441	5	AAO17874	Aao17874 C. glutami
166	39	41.5	328	8	ABM82567	Abm82567 Human dia	239	38	40.4	441	9	AEC56408	Aec56408 Corynebacc
167	39	41.5	328	8	ABM82568	Abm82568 Human dia	240	38	40.4	468	6	ABP79583	Abp79583 N. gonorr
168	39	41.5	361	4	ABB60382	Abb60382 Drosophil	241	38	40.4	505	7	ADJ71088	Adj71088 Human hea
169	39	41.5	376	2	AAR99254	Aar99254 Cytoplasm	242	38	40.4	585	4	AAU36330	Aau36330 Pseudomon

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:25:14 ; Search time 22.8 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-797-626-2

Perfect score: 94

Sequence: 1 KGGCSTQNAQLLSLVGKA 19

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR_80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	46.8	285	2	F04986
2	44	46.8	828	2	T23267
3	43	45.7	452	2	JG6507
4	42	44.7	71	2	T09239
5	42	44.7	1092	2	JX0312
6	41	43.6	240	2	S53403
7	41	43.6	263	2	S54719
8	41	43.6	428	2	A43741
9	41	43.6	476	1	JC2318
10	41	43.6	600	2	AE2570
11	41	43.6	643	2	AC2199
12	41	43.6	1401	2	T02255
13	41	43.6	2756	2	T30183
14	41	43.6	3295	2	A80074
15	40	42.6	425	2	C72744
16	40	42.6	436	2	G59466
17	40	42.6	556	2	E95289
18	40	42.6	617	2	T15408
19	40	42.6	624	2	T29286
20	40	42.6	772	2	T16474
21	40	42.6	1751	2	T09394
22	39.5	42.0	203	2	E75145
23	39.5	42.0	206	2	A71185
24	39.5	42.0	1811	2	T00035
25	39	41.5	139	2	D82296
26	39	41.5	227	2	D83162
27	39	41.5	269	2	B70124
28	39	41.5	361	2	T13745
29	39	41.5	376	2	B59273

30	39	41.5	437	2	AF0667	probable phosphotr
31	39	41.5	449	2	S78839	hypothetical prote
32	39	41.5	468	2	T08139	shaggy-like protei
33	39	41.5	476	2	AH2968	mannose-1-phosphat
34	39	41.5	476	2	C98314	mannose-1-phosphat
35	39	41.5	653	2	A84675	hypothetical prote
36	39	41.5	1049	1	S19421	ATP-dependent perm
37	39	41.5	1456	1	A36563	mannose receptor p
38	39	41.5	1499	2	A89813	glutamate synthase
39	39	41.5	1902	1	B44858	lactocepin (EC 3.4
40	39	41.5	2335	2	T40186	probable phosphati
41	38.5	41.0	820	2	T22172	hypothetical prote
42	38.5	41.0	1006	2	T00050	hypothetical prote
43	38	40.4	129	2	B83173	hypothetical prote
44	38	40.4	187	2	S32968	probable membrane
45	38	40.4	188	2	T52029	trpP kinase (EC 2.
46	38	40.4	195	2	H95297	probable allantoin
47	38	40.4	197	2	AB2571	hypothetical prote
48	38	40.4	244	2	F90801	HecB-like protein
49	38	40.4	273	2	T31892	hypothetical prote
50	38	40.4	348	2	G85661	hypothetical prote
51	38	40.4	357	2	D82337	UDP-N-acetylenolp
52	38	40.4	477	1	A29978	angiotensin precu
53	38	40.4	503	1	VMUT1B	variant surface gl
54	38	40.4	541	2	T43862	PAD flavoprotein o
55	38	40.4	546	2	AE0571	probable membrane
56	38	40.4	585	2	H83199	phosphotransferase
57	38	40.4	850	2	AE1954	hypothetical prote
58	38	40.4	907	2	T27317	hypothetical prote
59	38	40.4	928	2	T24868	hypothetical prote
60	38	40.4	1455	1	A48925	mannose receptor p
61	38	40.4	1902	2	S06997	lactocepin (EC 3.4
62	38	40.4	1902	2	B45764	lactocepin (EC 3.4
63	38	40.4	1962	2	A32634	lactocepin (EC 3.4
64	37.5	39.9	93	2	G70815	hypothetical prote
65	37	39.4	93	2	A86491	CT001 hypothetical
66	37	39.4	93	2	F72130	conserved hypothet
67	37	39.4	160	2	T25185	hypothetical prote
68	37	39.4	228	1	S18588	hypothetical mercu
69	37	39.4	237	2	B84377	hypothetical prote
70	37	39.4	267	2	S72583	abcl protein - Myc
71	37	39.4	288	1	JS0662	methylentetrahydr
72	37	39.4	288	2	B85553	5,10-methylene-tet
73	37	39.4	288	2	AB0344	methenyltetrahydro
74	37	39.4	288	2	G90702	5,10-methylene-tet
75	37	39.4	295	2	S56302	hypothetical prote
76	37	39.4	341	2	S69802	N-acetylmuramoyl-L
77	37	39.4	380	2	D84050	L-cysteine sulfurt
78	37	39.4	425	2	S03961	protein F53C3.11 [
79	37	39.4	457	2	S03961	Ig mu chain C regi
80	37	39.4	473	2	A86989	conserved hypothet
81	37	39.4	477	1	ANET	angiotensin precu
82	37	39.4	506	2	H82991	exopolysphatase
83	37	39.4	578	2	B37852	phosphotransferase
84	37	39.4	581	2	B81909	exodeoxyribonuclea
85	37	39.4	702	2	T16832	hypothetical prote
86	37	39.4	935	2	S62476	hypothetical prote
87	37	39.4	946	2	A84133	hypothetical prote
88	37	39.4	1095	2	T31423	polyprotein allierg
89	37	39.4	1097	2	S17308	leukemia inhibitor
90	37	39.4	1347	2	T02214	ubiquitous TPR mot
91	37	39.4	2823	2	F87908	protein T22A3.8 [i
92	37	39.4	2823	2	T23064	hypothetical prote
93	37	39.4	3102	2	T43291	laminin alpha chai
94	36.5	38.8	249	2	F96511	hypothetical prote
95	36.5	38.8	262	2	T17442	ybtP protein - yer
96	36.5	38.8	267	2	AH0232	yersiniabactin bio
97	36.5	38.8	267	2	T30344	irp4 protein - yer
98	36.5	38.8	267	2	T47050	hypothetical prote
99	36.5	38.8	342	2	AF3357	anthranilate phosph
100	36	38.3	55	2	B97548	hypothetical prote
101	36	38.3	76	2	AF2168	hypothetical prote
102	36	38.3	79	1	A58656	adipokinetic hormo

103	36	38.3	125	2	T27611	hypothetical prote	176	35	37.2	292	2	B95232	conserved hypothet
104	36	38.3	150	2	AH0371	probable membrane	177	35	37.2	293	2	F83618	conserved hypothet
105	36	38.3	178	2	G59856	hypothetical prote	178	35	37.2	294	2	T23682	hypothetical prote
106	36	38.3	227	2	E93288	probable ATP-bind	179	35	37.2	307	2	H71098	hypothetical prote
107	36	38.3	238	2	S77699	inner cell wall ma	180	35	37.2	309	2	AE0946	FdH protein limpo
108	36	38.3	260	2	D75404	phosphatidylglycer	181	35	37.2	317	2	G72342	L-isocaproate (D-a
109	36	38.3	261	2	I52518	sperm acrosome ant	182	35	37.2	323	2	C89045	protein B0238.6 [i
110	36	38.3	263	2	AE0140	molybdenum transpo	183	35	37.2	325	2	C71040	hypothetical prote
111	36	38.3	293	2	H70366	lysyl-tRNA synthet	184	35	37.2	333	2	F83107	hypothetical prote
112	36	38.3	321	2	D48560	immediate-early pr	185	35	37.2	334	2	G71979	probable type II D
113	36	38.3	321	2	JC5460	intracellular alka	186	35	37.2	344	1	KHFGD	cathepsin D (EC 3.
114	36	38.3	322	2	G83922	intracellular alka	187	35	37.2	381	2	T13701	NADH2 dehydrogenas
115	36	38.3	323	2	AB1596	hypothetical prote	188	35	37.2	385	2	A84646	probable serpin [i
116	36	38.3	329	2	T27337	hypothetical prote	189	35	37.2	391	2	B64606	acetyl coenzyme A
117	36	38.3	350	2	AC0037	probable tellurite	190	35	37.2	391	2	T32706	hypothetical prote
118	36	38.3	351	2	D82891	conserved hypothet	191	35	37.2	397	2	A96925	uncharacterized co
119	36	38.3	376	2	B1652	iron-sulfur cofact	192	35	37.2	423	2	B70931	probable PFB prote
120	36	38.3	384	2	AH0662	probable chemo-rec	193	35	37.2	430	2	T31155	hypothetical prote
121	36	38.3	384	2	D90547	oligopeptide ABC t	194	35	37.2	430	2	S77393	cell division prot
122	36	38.3	400	2	S76446	hypothetical prote	195	35	37.2	430	2	I39727	mannopine biosynth
123	36	38.3	425	2	T12473	hypothetical prote	196	35	37.2	431	2	T16191	hypothetical prote
124	36	38.3	447	2	C70951	hypothetical prote	197	35	37.2	442	2	T42048	mom-1 protein - Ca
125	36	38.3	469	2	A16660	nitrogenase vanadi	198	35	37.2	445	2	T38916	probable transcript
126	36	38.3	561	2	A11409	potassium-transpor	204	35	37.2	491	2	B96633	exoglucanase (EC 3
127	36	38.3	504	2	S09797	potassium-transpor	205	35	37.2	510	2	F90710	6-phosphogluconate
128	36	38.3	517	2	T04597	hypothetical prote	206	35	37.2	510	2	B64795	hypothetical prote
129	36	38.3	527	2	T38045	hypothetical prote	207	35	37.2	510	2	B85561	hypothetical prote
130	36	38.3	531	2	C97141	probable t-complex	208	35	37.2	535	2	T23419	citrate lyase alph
131	36	38.3	533	2	A86433	site-specific reco	209	35	37.2	537	2	T27612	hypothetical prote
132	36	38.3	561	2	A11409	TS18.19 protein -	210	35	37.2	558	2	B48492	polysaccharide exp
133	36	38.3	561	2	AH1785	potassium-transpor	211	35	37.2	558	2	I41324	hypothetical prote
134	36	38.3	567	2	E84658	hypothetical prote	212	35	37.2	563	2	T04598	polyisalic acid tr
135	36	38.3	614	2	A82832	protein-export mem	213	35	37.2	565	2	S10367	carboxylesterase (
136	36	38.3	747	2	A29229	two component resp	214	35	37.2	589	2	A82504	hypothetical prote
137	36	38.3	758	2	T02925	protoporphylin IX	215	35	37.2	601	2	T11677	probable transcript
138	36	38.3	775	1	EDBE11	immediate-early pr	216	35	37.2	610	2	S59558	dynammin-like prote
139	36	38.3	783	2	A98353	probable transcript	217	35	37.2	621	2	T15859	hypothetical prote
140	36	38.3	821	2	S67087	hypothetical prote	218	35	37.2	655	2	S54183	acyl-CoA dehydroge
141	36	38.3	835	1	S87669	transitional endop	219	35	37.2	658	2	C75187	anaerobic ribonuc
142	36	38.3	841	2	T14398	S-receptor kinase	220	35	37.2	681	2	T16353	hypothetical prote
143	36	38.3	997	2	A87320	TonB-dependent rec	221	35	37.2	686	2	T06700	hypothetical prote
144	36	38.3	1053	2	T30937	probable glycolipi	222	35	37.2	752	2	H90135	cell division cycl
145	36	38.3	1118	2	S57833	transmembrane prot	223	35	37.2	776	2	C83411	secretion protein
146	36	38.3	1206	2	T44376	DNA-directed RNA p	224	35	37.2	780	2	E69095	carbon monoxide de
147	36	38.3	1541	2	AC2474	heterocyst glycoli	225	35	37.2	787	2	G86436	hypothetical prote
148	36	38.3	1589	2	T13606	hypothetical prote	226	35	37.2	805	1	S19738	transitional endop
149	36	38.3	2021	2	AD2267	pyrimidine synthet	227	35	37.2	806	1	VPEG	transitional endop
150	36	38.3	2225	1	A23443	type I fatty acid	228	35	37.2	806	1	A55190	transitional endop
151	36	38.3	8243	2	T31307	germination respon	229	35	37.2	806	1	S25197	transitional endop
152	35.5	37.8	373	2	G69629	spore germination	230	35	37.2	806	1	T02243	probable transiti
153	35.5	37.8	549	2	S04845	ig heavy chain pre	231	35	37.2	819	2	JC7240	two-pore calcium c
154	35.5	37.8	62	2	H84255	tumor rejection an	232	35	37.2	829	2	A33166	colorectal tumor s
155	35	37.2	45	2	PC1154	hypothetical prote	233	35	37.2	906	2	T28034	hypothetical prote
156	35	37.2	62	2	H84255	hypothetical prote	234	35	37.2	912	2	G96830	hypothetical prote
157	35	37.2	67	2	H97845	hypothetical prote	235	35	37.2	952	2	T18900	disintegrin and me
158	35	37.2	98	2	A28918	hypothetical prote	236	35	37.2	995	2	A88483	protein C05P11.1 [
159	35	37.2	115	2	D81516	hypothetical prote	237	35	37.2	1041	2	T15521	hypothetical prote
160	35	37.2	116	2	E86633	hypothetical prote	238	35	37.2	1095	1	A31225	phospholipase C (E
161	35	37.2	177	2	T22603	hypothetical prote	239	35	37.2	1168	2	I56985	unknown protein, 4
162	35	37.2	185	2	H75168	2-ketoglutarate fe	240	35	37.2	1459	2	G86457	hemolysin (impor
163	35	37.2	185	2	D71046	probable ferredoxi	241	35	37.2	1635	2	A10452	adhesive ligand ep
164	35	37.2	199	2	F71462	hypothetical prote	242	35	37.2	1713	2	A55347	hypothetical prote
165	35	37.2	204	2	A81934	mercuric transport	243	35	37.2	2049	2	T29227	hypothetical prote
166	35	37.2	202	2	B69293	cellulose 1,4-beta	244	35	37.2	2241	2	T20971	pyrimidine synthet
167	35	37.2	228	2	S26995	molybdenum formylm	245	35	37.2	2242	2	A57541	hypothetical prote
168	35	37.2	231	2	H75076	hypothetical prote	246	35	37.2	2261	2	T20978	pyrimidine synthet
169	35	37.2	231	2	C97552	hypothetical prote	247	35	37.2	2591	1	S21010	filamentous hemagg
170	35	37.2	231	2	AD2772	hypothetical prote	248	35	37.2	4644	1	A38905	dynein heavy chain
171	35	37.2	235	2	G71658	hypothetical prote							
172	35	37.2	242	2	A80719	probable pertussis							
173	35	37.2	249	2	T27782	hypothetical prote							
174	35	37.2	256	2	A81354	glutamine-binding							
175	35	37.2	292	2	D98096	conserved hypothet							

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105	41	43.6	476	1	ANGT_SHEEP	P20757	ovis aries	178	40	42.6	556	2	Q930H5_RHIME	Q930H5 rhizobium m
106	41	43.6	600	2	Q8YJX0_ANASP	Q8YJX0	anabaena sp	179	40	42.6	596	2	Q3GF99_9FIRM	Q3GF99 syntrophomo
107	41	43.6	627	2	Q4E2E3_TRYCR	Q4E2E3	trypanosoma	180	40	42.6	601	2	Q2LVLO_9DELT	Q2LVLO syntrophus
108	41	43.6	643	2	Q8YSE2_ANASP	Q8YSE2	anabaena sp	181	40	42.6	617	1	CHIT_CAEEL	Q11174 caenorhabdi
109	41	43.6	728	2	Q8G12_FUSNN	Q8G12	fusobacteri	182	40	42.6	617	2	Q619N2_CABER	Q619N2 caenorhabdi
110	41	43.6	738	2	Q4CX81_TYCR	Q4CX81	trypanosoma	183	40	42.6	624	2	Q18448_CAEEL	Q18448 caenorhabdi
111	41	43.6	848	2	Q3M5K6_ANAVT	Q3M5K6	anabaena va	184	40	42.6	636	2	Q39Q98_GEOMG	Q39Q98 geobacter m
112	41	43.6	850	2	Q5SUC0_CRYNE	Q5SUC0	cryptococcu	185	40	42.6	686	2	Q2YBN8_NITMU	Q2YBN8 nitrospir
113	41	43.6	850	2	Q5K125_CRYNE	Q5K125	cryptococcu	186	40	42.6	701	2	Q5S955_XENLA	Q5S955 xenopus lae
114	41	43.6	880	2	Q8PSG7_COREP	Q8PSG7	corynebacte	187	40	42.6	701	2	Q6NIB7_XENLA	Q6NIB7 xenopus lae
115	41	43.6	991	2	Q4IQ25_GIBZE	Q4IQ25	gibberella	188	40	42.6	738	2	Q3EDA9_ARATH	Q3EDA9 arabidopsis
116	41	43.6	996	2	Q39QM4_GEOMG	Q39QM4	geobacter m	189	40	42.6	910	2	Q8Q915_ADEG8	Q8Q915 avian adeno
117	41	43.6	996	2	Q8R2W5_MOUSE	Q8R2W5	mus musculus	190	40	42.6	970	2	Q875T3_SACCA	Q875T3 saccharomyc
118	41	43.6	1035	2	Q86TD1_HUMAN	Q86TD1	homo sapien	191	40	42.6	971	2	Q2SSN2_MYCCA	Q2SSN2 mycoplasma
119	41	43.6	1141	2	Q54Q43_DICDI	Q54Q43	dictyosteli	192	40	42.6	990	2	Q75C45_ASHGO	Q75C45 ashbya goss
120	41	43.6	1150	2	Q6D180_MOUSE	Q6D180	mus musculus	193	40	42.6	1007	2	Q4AS60_9BURK	Q4AS60 polaromonas
121	41	43.6	1236	2	Q38R75_TRYPAN	Q38R75	trypanosoma	194	40	42.6	1048	2	Q8W517_IPOBA	Q8W517 ipomoea bat
122	41	43.6	1288	2	Q38R75_TRYPAN	Q38R75	trypanosoma	195	40	42.6	1222	2	Q4RT35_TPOBA	Q4RT35 tetraodon n
123	41	43.6	1288	2	Q38R75_TRYPAN	Q38R75	trypanosoma	196	40	42.6	1282	2	Q4RT35_TPOBA	Q4RT35 tetraodon n
124	41	43.6	1333	1	UTX_MOUSE	UTX_MOUSE	mus musculus	197	40	42.6	1498	2	Q4QJ11_LEIMA	Q4QJ11 leishmania
125	41	43.6	1401	1	UTX_MOUSE	UTX_MOUSE	mus musculus	198	40	42.6	1506	2	Q8CMR9_STAES	Q8CMR9 staphylococ
126	41	43.6	1401	2	Q52LL9_HUMAN	Q52LL9	homo sapien	199	40	42.6	1510	2	Q4L3C8_STAHL	Q4L3C8 staphylococ
127	41	43.6	1401	2	Q5JUV43_HUMAN	Q5JUV43	homo sapien	200	40	42.6	1510	2	Q9Z465_CORGL	Q9Z465 corynebacte
128	41	43.6	1406	2	Q59HG3_HUMAN	Q59HG3	homo sapien	201	40	42.6	1522	2	Q8NTW8_CORGL	Q8NTW8 corynebacte
129	41	43.6	1424	2	Q7TSG4_MOUSE	Q7TSG4	mus musculus	202	40	42.6	1751	2	Q2PYF9_9BACT	Q2PYF9 uncultured
130	41	43.6	1455	2	Q6AZS3_XENLA	Q6AZS3	xenopus lae	203	40	42.6	2531	2	Q92815_9RETR	Q92815 walleye der
131	41	43.6	2064	2	Q8B6R7_9RHAB	Q8B6R7	flanders vi	204	40	42.6	2531	2	Q8EGK0_SHEON	Q8EGK0 shewanella
132	41	43.6	2664	2	Q3P4K1_9GAMM	Q3P4K1	shewanella	205	40	42.6	2581	2	Q93CG8_PHOPR	Q93CG8 photobacter
133	41	43.6	2756	2	Q33904_9GAMM	Q33904	shewanella	206	40	42.6	2619	2	Q6LS55_PHOPR	Q6LS55 photobacter
134	41	43.6	3295	2	Q74RUS_YERPE	Q74RUS	yersinia pe	207	40	42.6	2624	2	Q33TP3_9GAMM	Q33TP3 shewanella
135	41	43.6	3295	2	Q8Z1A8_YERPE	Q8Z1A8	yersinia pe	208	40	42.6	2624	2	Q368M8_9GAMM	Q368M8 shewanella
136	40.5	43.1	3378	2	Q66506_YERPL	Q66506	yersinia ps	209	40	42.6	2640	2	Q35ZQ6_9GAMM	Q35ZQ6 shewanella
137	40.5	43.1	254	2	Q5WMS2_LEGPL	Q5WMS2	legionella	210	40	42.6	2642	2	Q2ZRO9_SHEPU	Q2ZRO9 shewanella
138	40.5	43.1	254	2	Q3X5D2_LEGPA	Q3X5D2	legionella	211	40	42.6	2644	2	Q2X787_9GAMM	Q2X787 shewanella
139	40.5	43.1	332	2	Q8NV74_CORGL	Q8NV74	corynebacte	212	40	42.6	2657	2	Q2Z774_9GAMM	Q2Z774 shewanella
140	40.5	43.1	368	2	Q3FT34_9BURK	Q3FT34	rhodoferr	213	40	42.6	2693	2	Q3Q6R8_9GAMM	Q3Q6R8 shewanella
141	40.5	43.1	483	2	Q30B58_ACIG3	Q30B58	acinetobact	214	39.5	42.0	203	1	RLI8_PVRAB	RLI8 pyrococcus
142	40.5	43.1	587	2	Q9JX9_PLAGA	Q9JX9	plasmodium	215	39.5	42.0	203	1	RLI8_PVRHU	RLI8 pyrococcus
143	40.5	43.1	891	2	Q36N24_MARHY	Q36N24	marinobacte	216	39.5	42.0	333	1	TRPD_PASMU	TRPD pasteurella
144	40	42.6	87	2	Q3IKR8_PSEHT	Q3IKR8	pseudocalt	217	39.5	42.0	798	2	Q6ZC60_ORYSA	Q6ZC60 oryza sativ
145	40	42.6	209	2	Q48V17_STRPM	Q48V17	streptococc	218	39.5	42.0	847	2	Q2R0C6_ORYSA	Q2R0C6 oryza sativ
146	40	42.6	209	2	Q8KH0_STRP3	Q8KH0	streptococc	219	39.5	42.0	933	2	Q61WH7_HUMAN	Q61WH7 homo sapien
147	40	42.6	209	2	Q9A184_STRP1	Q9A184	streptococc	220	39.5	42.0	1288	2	Q54M67_DICDI	Q54M67 dictyosteli
148	40	42.6	213	2	Q8GVF4_ORYSA	Q8GVF4	oryza sativ	221	39.5	42.0	1811	2	Q36184_9VIRU	Q36184 plautia sta
149	40	42.6	219	2	Q2YZU2_9DELT	Q2YZU2	uncultured	222	39.5	42.0	2180	2	Q9VAS8_DROME	Q9VAS8 drosophila
150	40	42.6	230	2	Q3A158_BACTN	Q3A158	synecococc	223	39.5	42.0	3966	2	Q7KVA7_DROME	Q7KVA7 drosophila
151	40	42.6	231	2	Q8A1G6_BACTN	Q8A1G6	bacteroides	224	39.5	42.0	36	2	Q700Q9_PIG	Q700Q9 sus scrofa
152	40	42.6	255	2	Q39CF2_BURS3	Q39CF2	burkholderi	225	39	41.5	37	2	Q8DVG1_STRMU	Q8DVG1 streptococc
153	40	42.6	275	2	Q7XL00_ORYSA	Q7XL00	oryza sativ	226	39	41.5	78	2	Q8DJA7_SYNEL	Q8DJA7 synecococc
154	40	42.6	292	2	Q3MH5_BOVIN	Q3MH5	bos taurus	227	39	41.5	125	2	Q31L13_SYNEP7	Q31L13 synecococc
155	40	42.6	302	2	Q35NZ2_9BRAD	Q35NZ2	bradyrhizob	228	39	41.5	131	2	Q4ZW35_PSEU2	Q4ZW35 pseudomonas
156	40	42.6	311	2	Q3NDL6_9PROT	Q3NDL6	nitrosomona	229	39	41.5	139	2	Q9KU74_VIBCH	Q9KU74 vibrio chol
157	40	42.6	322	2	Q656F5_ORYSA	Q656F5	oryza sativ	230	39	41.5	147	2	Q33JS4_METHU	Q33JS4 methanospir
158	40	42.6	330	2	Q7PNF1_ANOGA	Q7PNF1	anopheles g	231	39	41.5	152	2	Q3G7H3_9DELT	Q3G7H3 pelobacter
159	40	42.6	331	2	Q4NLB8_9MICC	Q4NLB8	arthrobacte	232	39	41.5	163	2	Q5SP45_MOUSE	Q5SP45 mus musculu
160	40	42.6	334	2	Q30389_PSEAE	Q30389	pseudomonas	233	39	41.5	171	2	Q2SG77_9GAMM	Q2SG77 habella che
161	40	42.6	334	2	Q31E51_THICR	Q31E51	thiomicrosp	234	39	41.5	184	2	Q9FXS4_TOHAC	Q9FXS4 nicotiana t
162	40	42.6	334	2	Q8RI15_FUSNN	Q8RI15	fusobacteri	235	39	41.5	195	2	Q3N8G5_9PROT	Q3N8G5 nitrosomona
163	40	42.6	353	2	Q415V6_GIBZE	Q415V6	gibberella	236	39	41.5	205	2	Q5QSY9_9LACO	Q5QSY9 lactobacill
164	40	42.6	368	2	Q9AB3_RHILO	Q9AB3	rhizobium l	237	39	41.5	205	2	Q6BVM3_DEBHA	Q6BVM3 debaryomyce
165	40	42.6	372	2	Q3PHR7_PARDE	Q3PHR7	paracoccu	238	39	41.5	208	2	Q94306_BACFI	Q94306 bacillus fi
166	40	42.6	388	2	Q3FR59_9BURK	Q3FR59	rhodoferr	239	39	41.5	209	2	Q8P2A4_STRP8	Q8P2A4 streptococc
167	40	42.6	394	2	Q5S1X0_IXOSC	Q5S1X0	ixodes scap	240	39	41.5	209	2	Q5XDL5_STRP6	Q5XDL5 streptococc
168	40	42.6	396	2	Q3MZK3_9DELT	Q3MZK3	syntriphoba	241	39	41.5	225	2	Q41QS9_FERAC	Q41QS9 ferroplasma
169	40	42.6	409	2	Q4T9R3_TETNG	Q4T9R3	tetraodon n	242	39	41.5	226	2	Q590H1_ATEGE	Q590H1 ateles geof
170	40	42.6	425	2	Q9YEU9_AERPE	Q9YEU9	aeropyrum p	243	39	41.5	226	2	Q5F0X4_PSEFL	Q5F0X4 pseudomonas
171	40	42.6	428	2	Q2JMU3_9CVAN	Q2JMU3	cyanobacter	244	39	41.5	227	2	Q54046_PSEAE	Q54046 pseudomonas
172	40	42.6	428	2	Q2JU94_9CVAN	Q2JU94	cyanobacter	245	39	41.5	231	2	Q3RV16_RALME	Q3RV16 ralstonia m
173	40	42.6	436	1	HMDH_ARCFU	HMDH_ARCFU	archaeoglob	246	39	41.5	239	2	Q65215_RAT	Q65215 rattus norv
174	40	42.6	477	2	Q3VCN0_MOUSE	Q3VCN0	mus musculu	247	39	41.5	246	2	Q7SCW1_NEUCR	Q7SCW1 neurospora
175	40	42.6	482	2	Q3UTR7_MOUSE	Q3UTR7	mus musculu	248	39	41.5	247	1	PYRF_CHRVO	PYRF chromobacte
176	40	42.6	501	2	Q622M8_CABER	Q622M8	caenorhabdi	249	39	41.5	261	2	Q9G918_OCHDN	Q9G918 ochromonas
177	40	42.6	508	2	Q56V70_9ROSI	Q56V70	thecacaris	250	39	41.5				

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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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- 2: /EMC_Celerra_SID33/prodata/2/iaa/6 COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	43	45.7	260	2	US-09-989-903-55
6	43	45.7	751	2	US-10-020-079-8
7	43	45.7	751	2	US-10-413-437-8
8	43	45.7	764	2	US-10-413-437-6
9	43	45.7	764	2	US-10-020-079-24
10	43	45.7	776	2	US-10-413-437-24
11	43	45.7	789	2	US-10-020-079-22
12	43	45.7	789	2	US-10-413-437-22
13	43	45.7	838	2	US-10-020-079-40
14	43	45.7	838	2	US-10-413-437-40
15	43	45.7	851	2	US-10-020-079-38
16	43	45.7	851	2	US-10-413-437-38
17	43	45.7	863	2	US-10-020-079-32
18	43	45.7	863	2	US-10-413-437-32
19	43	45.7	864	2	US-10-020-079-4
20	43	45.7	864	2	US-10-413-437-4
21	43	45.7	870	2	US-10-020-079-2
22	43	45.7	870	2	US-10-413-437-2
23	43	45.7	876	2	US-10-020-079-30
24	43	45.7	876	2	US-10-413-437-30
25	43	45.7	889	2	US-10-020-079-20
26	43	45.7	889	2	US-10-413-437-20

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28	43	45.7	895	2	US-10-020-079-18	Sequence 18, Appl
29	43	45.7	895	2	US-10-413-437-18	Sequence 18, Appl
30	43	45.7	951	2	US-10-020-079-36	Sequence 36, Appl
31	43	45.7	951	2	US-10-413-437-36	Sequence 36, Appl
32	43	45.7	957	2	US-10-020-079-34	Sequence 34, Appl
33	43	45.7	957	2	US-10-413-437-34	Sequence 34, Appl
34	43	45.7	976	2	US-10-020-079-28	Sequence 28, Appl
35	43	45.7	976	2	US-10-413-437-28	Sequence 28, Appl
36	43	45.7	982	2	US-10-020-079-26	Sequence 26, Appl
37	43	45.7	982	2	US-10-413-437-26	Sequence 26, Appl
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41	41	43.6	2756	1	US-08-375-709-11	Sequence 11, Appl
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43	41	43.6	2756	2	US-09-090-793-7	Sequence 7, Appl
44	41	43.6	2756	2	US-09-231-899-7	Sequence 7, Appl
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52	39	41.5	70	2	US-09-289-346B-10	Sequence 10, Appl
53	39	41.5	297	2	US-09-134-000C-4187	Sequence 4187, Ap
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55	39	41.5	376	1	US-08-385-500-4	Sequence 4, Appl
56	39	41.5	376	1	US-08-846-784-4	Sequence 4, Appl
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58	39	41.5	674	2	US-08-653-648A-14	Sequence 14, Appl
59	39	41.5	675	2	US-09-564-418-12	Sequence 12, Appl
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61	39	41.5	1049	2	US-09-538-032-72	Sequence 72, Appl
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69	38	40.4	174	2	US-09-270-767-47768	Sequence 47768, A
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76	38	40.4	519	2	US-09-270-767-51255	Sequence 51255, A
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87	37	39.4	109	2	US-09-438-185A-2	Sequence 2, Appl
88	37	39.4	136	2	US-09-710-279-912	Sequence 912, App
89	37	39.4	154	2	US-09-489-039A-11527	Sequence 11527, A
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91	37	39.4	248	2	US-09-482-273-126	Sequence 126, App
92	37	39.4	272	1	US-08-690-095-1	Sequence 1, Appl
93	37	39.4	272	2	US-09-113-789-1	Sequence 1, Appl
94	37	39.4	295	2	US-09-538-092-281	Sequence 281, App
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99	37	39.4	557	2	US-09-252-991A-22750	Sequence 22750, A

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102	37	39.4	984	2	US-09-171-461-14	Sequence 14, Appl	175	35	37.2	308	2	US-09-149-476-607	Sequence 607, Ap
103	37	39.4	984	2	US-09-970-711-14	Sequence 14, Appl	176	35	37.2	309	2	US-09-489-039A-12224	Sequence 12224, A
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108	37	39.4	1067	2	US-09-107-532A-5148	Sequence 5148, Ap	181	35	37.2	348	2	US-09-270-767-44163	Sequence 44163, A
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111	37	39.4	1097	1	US-08-347-003-6	Sequence 6, Appli	184	35	37.2	399	2	US-09-248-796A-20092	Sequence 20092, A
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116	37	39.4	1347	2	US-09-058-489-24	Sequence 24, Appl	189	35	37.2	441	2	US-09-149-476-372	Sequence 372, App
117	37	39.4	2158	2	US-10-144-198-34	Sequence 34, Appl	190	35	37.2	467	2	US-09-252-991A-23257	Sequence 23257, A
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124	36.5	38.8	3174	1	US-08-477-451-3	Sequence 3, Appli	197	35	37.2	806	2	US-09-949-016-6786	Sequence 6786, Ap
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134	36	38.3	262	1	US-08-292-045-11	Sequence 11, Appl	207	35	37.2	829	1	US-09-270-767-42739	Sequence 42739, A
135	36	38.3	285	2	US-09-252-991A-26081	Sequence 26081, A	208	35	37.2	908	2	US-09-489-039A-13928	Sequence 13928, A
136	36	38.3	288	2	US-09-949-016-6985	Sequence 6985, Ap	209	35	37.2	926	2	US-08-993-228-19	Sequence 19, Appl
137	36	38.3	310	2	US-10-104-047-3795	Sequence 3795, Ap	210	35	37.2	1075	1	US-10-771-708-10	Sequence 10, Appl
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142	36	38.3	514	2	US-09-902-540-10406	Sequence 10406, A	215	35	37.2	1713	2	US-09-538-032-1359	Sequence 1359, Ap
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144	36	38.3	561	2	US-09-270-767-56367	Sequence 56367, A	217	35	37.2	1724	2	US-09-560-385A-2	Sequence 2, Appli
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146	36	38.3	758	2	US-09-403-463A-2	Sequence 2, Appli	219	35	37.2	3854	2	US-09-949-016-7876	Sequence 7876, Ap
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152	35	37.2	29	2	US-06-256-204C-66	Sequence 66, Appl	225	34.5	36.7	112	2	US-09-766-396-2	Sequence 2, Appli
153	35	37.2	32	2	US-08-149-476-740	Sequence 740, App	226	34.5	36.7	112	2	US-09-893-737-188	Sequence 188, App
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158	35	37.2	85	2	US-09-270-767-59587	Sequence 59587, A	231	34	36.2	69	2	US-08-995-159-3	Sequence 3, Appli
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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:32:28 ; Search time 19.76 Seconds
(without alignments)
67.548 Million cell updates/sec

Title: US-10-797-626-2

Perfect score: 94

Sequence: 1 KGCSTQNAQLSLIVCKA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	40	42.6	213	6	US-10-953-349-28900
6	40	42.6	213	7	US-11-056-355B-62667
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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:11:07 ; Search time 133.56 Seconds
(without alignments)
61.619 Million cell updates/sec

Title: US-10-797-626-3

Perfect score: 85

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Scoring table: BLOSUM62

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Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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8: Geneseq2004s:*

9: Geneseq2005s:*

10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	85	100.0	18	ADS18079	Adsl8079 Laminin s
2	74.5	87.6	19	ADS18078	Adsl8078 Laminin s
3	44	51.8	148	AAB80171	Aab80171 Corynebact
4	44	51.8	148	AAG93238	Aag93238 C Glutami
5	44	51.8	204	ADN47346	Adn47346 Thermococ
6	43	50.6	13	ADS18077	Adsl8077 Laminin s
7	43	50.6	313	AAV34857	Aav34857 Chlamydia
8	41	48.2	127	AAB11673	Aab11673 A. vitis
9	41	48.2	151	AAK90552	Aak90552 pJG4-5-CD
10	41	48.2	272	AAB11676	Aab11676 A. vitis
11	41	48.2	298	AAV36978	Aav36978 Amino aci
12	41	48.2	298	ABU27101	Abu27101 Protein e
13	41	48.2	512	ADS25034	Ad25034 Bacterial
14	41	48.2	547	ADY05403	Ady05403 Plant ful
15	41	48.2	560	ADX96685	Adx96685 Plant ful
16	41	48.2	562	ADX96686	Adx96686 Plant ful
17	41	48.2	1399	ABU41685	Abu41685 Protein e
18	41	48.2	1634	RAA42452	Raa42452 Enzyme in
19	41	48.2	1642	AAW89400	Aaw89400 S. putref
20	41	48.2	2756	AAW99462	Aaw99462 Biosynthe
21	41	48.2	2756	AAW37050	Aaw37050 S. putref
22	41	48.2	2756	3 AAB10467	Aab10467 Shewanell
23	41	48.2	2756	4 AAG64455	Aag64455 S. putref

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26	40	47.1	70	5	ABP08060	Abp08060 Human ORF
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28	40	47.1	337	4	ABU43424	Abu43424 Protein e
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32	40	47.1	389	6	ABU42490	Abu42490 Protein e
33	40	47.1	397	4	AAU37106	Aau37106 Staphyloc
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35	40	47.1	652	7	ABM88164	Abm88164 Rice abio
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45	39	45.9	227	6	ABU38639	Abu38639 Protein e
46	39	45.9	353	8	ADK69718	Adk69718 Rhizopus
47	39	45.9	357	8	ADK69725	Adk69725 Rhizopus
48	39	45.9	377	8	ADT59035	Adt59035 Plant pol
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53	39	45.9	54	8	ADK47824	Adk47824 Streptoco
54	38	44.7	63	8	ADK96135	Adk96135 Novel S.
55	38	44.7	63	9	AEA60005	Aea60005 Streptoco
56	38	44.7	96	4	AAU47148	Aau47148 Protein e
57	38	44.7	131	6	ABP28278	Abp28278 Streptoco
58	38	44.7	136	5	ABO65010	AbO65010 Klebsiell
59	38	44.7	154	8	ADX75550	Adx75550 Plant ful
60	38	44.7	203	4	AAU41181	Aau41181 Protein e
61	38	44.7	246	8	ADK97068	Adk97068 Plant ful
62	38	44.7	274	6	ADU06917	AdU06917 Bacterial
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64	38	44.7	312	7	ABO80324	AbO80324 Pseudomon
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66	38	44.7	438	8	ADJ49185	Adj49185 Oil-assoc
67	38	44.7	468	6	ABP79583	Abp79583 N. gonorr
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71	38	44.7	645	4	ABG82945	Abg82945 S. epider
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73	38	44.7	739	5	ABG80351	Abg80351 Clostridi
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75	38	44.7	1004	6	ABU29133	Abu29133 Protein e
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80	38	44.7	1778	4	ABE60081	AbE60081 Drosophil
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84	37	43.5	19	4	AAU18519	Aau18519 Peptide #
85	37	43.5	19	4	AAU18519	Aau18519 Peptide #
86	37	43.5	19	4	AAU18519	Aau18519 Peptide #
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91	37	43.5	57	5	ADP07642	Adp07642 Human ORF
92	37	43.5	72	4	AAU44084	Aau44084 Propionib
93	37	43.5	72	6	ABM40603	Abm40603 Propionib
94	37	43.5	224	3	ABG20878	Abg20878 Arabidops
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101	35	37.2	248	6	US-10-953-349-38275	Sequence 38275, A	174	34	36.2	161	6	US-10-953-349-9518	Sequence 9518, Ap
102	35	37.2	298	7	US-11-056-355B-10463	Sequence 10463, A	175	34	36.2	164	6	US-10-953-349-9517	Sequence 9517, Ap
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158	35	37.2	1313	6	US-10-953-349-9733	Sequence 9733, Ap	231	34	36.2	528	7	US-11-056-355B-82342	Sequence 82342, A
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160	35	37.2	1511	6	US-10-953-349-9731	Sequence 9731, Ap	233	34	36.2	531	6	US-10-449-902-44583	Sequence 44583, A
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162	35	37.2	2304	6	US-10-540-898-310	Sequence 310, App	235	34	36.2	531	6	US-10-449-902-52856	Sequence 52856, A
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166	34.5	36.7	350	6	US-10-449-902-51276	Sequence 51276, A	239	34	36.2	609	7	US-11-056-355B-66292	Sequence 66292, A
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168	34.5	36.7	561	7	US-11-330-403-558	Sequence 558, App	241	34	36.2	627	7	US-11-056-355B-72459	Sequence 72459, A
169	34	36.2	69	6	US-10-449-902-54631	Sequence 54631, A	242	34	36.2	627	7	US-11-330-403-278	Sequence 278, App
170	34	36.2	91	7	US-11-331-240-24	Sequence 24, Appl	243	34	36.2	628	6	US-10-449-902-52932	Sequence 52932, A
171	34	36.2	133	6	US-10-953-349-11905	Sequence 11905, A	244	34	36.2	642	7	US-11-056-355B-46723	Sequence 46723, A

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97	37	43.5	254	Aeb39665	L. pneumo	170	36	42.4	164	5	ABP29430	Streptoco
98	37	43.5	261	AGB36245	L. pneumo	171	36	42.4	170	8	ADV89055	Streptoco
99	37	43.5	263	AGS0880	Arabidops	172	36	42.4	170	8	ADV80308	Streptoco
100	37	43.5	262	AGS20877	Arabidops	173	36	42.4	173	4	AUA48434	Propionib
101	37	43.5	282	ADC95926	E. faeciu	174	36	42.4	173	6	ABM44953	Propionib
102	37	43.5	330	ADN47924	Thermoco	175	36	42.4	182	8	ADY23635	Plant ful
103	37	43.5	345	ADC23783	Protein s	176	36	42.4	188	8	ADV82426	Streptoco
104	37	43.5	345	ADH35884	Chemical	177	36	42.4	200	4	AGG91344	C. glutami
105	37	43.5	345	AGD93585	Nitrilase	178	36	42.4	214	2	AAJ34657	C. pneumo
106	37	43.5	345	ADI62182	Nitrilase	179	36	42.4	224	4	ABG08992	Novel hum
107	37	43.5	345	ADI64303	C. glutami	180	36	42.4	224	7	ABO68854	Pseudomon
108	37	43.5	381	AGS89795	C. glutami	181	36	42.4	243	4	AAU54529	Propionib
109	37	43.5	388	AAW26740	Staphyloc	182	36	42.4	243	6	ABM51048	Propionib
110	37	43.5	400	ABM68527	Photorhab	183	36	42.4	247	8	ADX94323	Plant ful
111	37	43.5	431	ABT79671	Corynebac	184	36	42.4	257	7	ABO78861	Pseudomon
112	37	43.5	441	AAO17874	C. glutami	185	36	42.4	263	8	ADY08521	Plant ful
113	37	43.5	441	AEC56408	Corynebac	186	36	42.4	272	4	AGY92867	C. glutami
114	37	43.5	477	ADY09358	Plant ful	187	36	42.4	274	4	ABT79597	Corynebac
115	37	43.5	518	ADW18497	Pinus rad	188	36	42.4	276	5	ABB89125	Human pol
116	37	43.5	534	ABG63970	Drosophil	189	36	42.4	276	8	ADY22862	Plant ful
117	37	43.5	547	ABB91886	Hexibicida	190	36	42.4	278	6	ABU25195	Protein e
118	37	43.5	548	ABB63196	Drosophil	191	36	42.4	285	7	ABO77335	Pseudomon
119	37	43.5	553	ADG74149	Rat prost	192	36	42.4	289	4	ABM80029	Corynebac
120	37	43.5	559	ADM04660	Human pro	193	36	42.4	289	4	ABT79596	Corynebac
121	37	43.5	559	ADM04658	Human pro	194	36	42.4	289	7	ADD13551	C. glutam
122	37	43.5	559	AEC87590	Human cDN	195	36	42.4	289	7	ADD13707	C. glutam
123	37	43.5	559	AEC87588	Human cDN	196	36	42.4	289	7	ADD13405	C. glutam
124	37	43.5	560	AGG67397	Amino aci	197	36	42.4	289	9	AEC56314	Corynebac
125	37	43.5	613	AAW60593	Cladospor	198	36	42.4	290	7	ADF06696	Bacterial
126	37	43.5	665	ABP65389	Flidobac	199	36	42.4	290	7	ADH86302	Enterococ
127	37	43.5	868	ABG24427	Novel hum	200	36	42.4	313	4	AAJ91515	Listeria
128	37	43.5	886	ADS24527	Bacterial	201	36	42.4	341	2	AAJ91515	Listeria
129	37	43.5	886	ADS29177	Bacterial	202	36	42.4	348	7	ADH87511	Enterococ
130	37	43.5	896	ADF05154	Bacterial	203	36	42.4	355	7	ADB65402	Human pro
131	37	43.5	1079	AAW81504	Short for	204	36	42.4	394	7	ADC95557	E. faeciu
132	37	43.5	1240	AAW81505	Medium fo	205	36	42.4	413	3	AAU42399	Arabidops
133	37	43.5	1347	AAW81506	Long form	206	36	42.4	425	4	AAU59756	Propionib
134	37	43.5	1450	ADA89491	Staphyloc	207	36	42.4	425	6	ABM56275	Propionib
135	37	43.5	1491	AAU34072	Staphyloc	208	36	42.4	428	6	ABU33541	Protein e
136	37	43.5	1499	ABU16457	Protein e	209	36	42.4	431	6	ABU49807	Protein e
137	37	43.5	1502	AAU36569	Staphyloc	210	36	42.4	432	4	AAU34681	E. coli c
138	37	43.5	1502	ABM71608	Staphyloc	211	36	42.4	432	4	AAU38273	Salmonell
139	37	43.5	1509	ABU43942	Protein e	212	36	42.4	432	6	ABU27856	Protein e
140	37	43.5	1510	AAJ01312	Glutamine	213	36	42.4	432	6	ABU48163	Protein e
141	37	43.5	1510	AAAB79669	Corynebac	214	36	42.4	432	6	ABU28736	Protein e
142	37	43.5	1510	AAG89953	C. glutami	215	36	42.4	432	6	ABU45604	Protein e
143	37	43.5	1510	ADD13595	C. glutam	216	36	42.4	432	6	ABU32200	Protein e
144	37	43.5	1560	AAJ94145	S. cremor	217	36	42.4	432	8	ADS45097	Bacterial
145	37	43.5	1959	AAAR10562	Mutant pr	218	36	42.4	432	9	ABE14273	E. coli e
146	37	43.5	1962	AAAR10558	Mutant pr	219	36	42.4	432	9	ABE94082	Escherich
147	37	43.5	1962	AAAR10559	Mutant pr	220	36	42.4	433	6	ABU39502	Protein e
148	37	43.5	1962	AAAR10557	Mutant pr	221	36	42.4	433	6	ABU40605	Protein e
149	37	43.5	1962	AAAR10563	Mutant pr	222	36	42.4	433	6	ABU49553	Protein e
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151	37	43.5	1962	AAAR10560	Mutant pr	224	36	42.4	433	8	ADN17516	Bacterial
152	37	43.5	1968	AAAR10941	Mutant pr	225	36	42.4	434	6	ABM70267	Phototrab
153	37	43.5	1974	AAAR10940	Mutant pr	226	36	42.4	436	4	AAU35561	Haemophil
154	37	43.5	2071	ABG17955	Novel hum	227	36	42.4	436	6	ABU30433	Protein e
155	37	43.5	2625	AAAB23832	Shewanell	228	36	42.4	456	7	ADF05805	Bacterial
156	37	43.5	2652	AAAG78664	Moritella	229	36	42.4	459	3	ABO63544	Klebsiell
157	37	43.5	2823	ADN22567	Bacterial	230	36	42.4	498	3	AAJ42398	Arabidops
158	37	43.5	2823	ADN22568	Bacterial	231	36	42.4	506	8	ADB82744	Human pro
159	37	43.5	6291	ADJ23927	Streptomy	232	36	42.4	506	8	ABM81174	Tumour-as
160	36.5	42.9	306	ADC96291	E. faeciu	233	36	42.4	511	9	ABE40306	L. pneumo
161	36.5	42.9	404	ADB86308	Aspergill	234	36	42.4	522	8	ABT94745	Plant ful
162	36	42.4	52	ABM64733	Propionib	235	36	42.4	525	4	ABG13978	Novel hum
163	36	42.4	60	ADP55226	Human PRO	236	36	42.4	533	5	ABE91198	Herbicida
164	36	42.4	60	ADY18398	PRO polyP	237	36	42.4	538	9	ABE36945	L. pneumo
165	36	42.4	64	ABE68023	Drosophil	238	36	42.4	548	8	ADM99141	Environme
166	36	42.4	109	AAO60004	Human pol	239	36	42.4	557	7	ABO74004	Pseudomon
167	36	42.4	114	ADK36128	Novel hum	240	36	42.4	585	4	AAU36330	Pseudomon
168	36	42.4	115	AAU27821	Chinese h	241	36	42.4	585	6	ABU38569	Protein e
169	36	42.4	155	AAJ73048	Olfactory	242	36	42.4	591	7	ABR84528	Drosophil

101	40	42.6	645	5	US-10-793-626-2384	Sequence 2984, Ap	174	38	40.4	91	4	US-10-437-963-136678	Sequence 136678,
102	40	42.6	933	4	US-10-282-122A-71028	Sequence 71028, A	175	38	40.4	112	4	US-10-425-115-275596	Sequence 275596,
103	40	42.6	1501	5	US-10-793-626-2850	Sequence 2850, Ap	176	38	40.4	117	4	US-10-135-545A-12	Sequence 12, Appl
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105	40	42.6	1510	3	US-09-738-626-3707	Sequence 3707, Ap	178	38	40.4	117	6	US-11-076-728-12	Sequence 33413,
106	40	42.6	1510	5	US-10-494-675-162	Sequence 162, Ap	179	38	40.4	121	4	US-10-425-115-334413	Sequence 250984,
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112	39.5	42.0	206	5	US-10-732-923-4076	Sequence 4076, Ap	185	38	40.4	316	3	US-09-795-271-51	Sequence 4, Appl
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122	39	41.5	70	4	US-10-633-850-11	Sequence 11, Appl	195	38	40.4	430	6	US-11-096-568A-23788	Sequence 271282,
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124	39	41.5	87	3	US-09-764-891-3657	Sequence 3657, Ap	197	38	40.4	441	3	US-10-721-922A-116	Sequence 116, App
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132	39	41.5	309	4	US-10-087-192-738	Sequence 738, App	205	38	40.4	630	4	US-10-437-963-125447	Sequence 125447,
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136	39	41.5	376	3	US-09-993-363-2	Sequence 2, Appl	209	38	40.4	812	4	US-09-908-193-35	Sequence 35, Appl
137	39	41.5	376	4	US-10-782-401-9	Sequence 9, Appl	210	38	40.4	891	4	US-10-128-714-8601	Sequence 8601, Ap
138	39	41.5	376	5	US-10-370-715B-4	Sequence 4, Appl	211	38	40.4	912	4	US-10-128-714-8092	Sequence 8092, Ap
139	39	41.5	376	5	US-10-501-035-283	Sequence 283, App	212	38	40.4	815	5	US-10-732-923-23238	Sequence 23238, A
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143	39	41.5	582	6	US-11-097-143-18753	Sequence 18753, A	216	38	40.4	1233	4	US-10-388-470-7	Sequence 7, Appl
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149	39	41.5	1456	3	US-09-870-759-95	Sequence 95, Appl	222	38	40.4	1479	4	US-10-408-765A-2212	Sequence 2212, App
150	39	41.5	1456	3	US-09-751-708A-95	Sequence 95, Appl	223	38	40.4	1479	4	US-10-474-794-238	Sequence 238, App
151	39	41.5	1456	4	US-10-293-027-1217	Sequence 1217, Ap	224	38	40.4	1479	5	US-10-618-281-67	Sequence 67, Appl
152	39	41.5	1456	4	US-10-428-817A-91	Sequence 91, Appl	225	38	40.4	1479	5	US-10-723-860-3515	Sequence 3515, Ap
153	39	41.5	1456	5	US-10-723-860-673	Sequence 673, App	226	38	40.4	1479	5	US-10-703-817-9	Sequence 9, Appl
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155	39	41.5	1491	3	US-09-815-242-5568	Sequence 5568, Ap	228	38	40.4	1479	5	US-10-840-590-20	Sequence 20, Appl
156	39	41.5	1499	4	US-10-282-122A-44381	Sequence 44381, A	229	38	40.4	1545	5	US-10-732-923-2248	Sequence 2248, Ap
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158	39	41.5	2335	4	US-10-425-115-239208	Sequence 239208, A	231	38	40.4	1734	4	US-10-126-148-6	Sequence 6, Appl
159	39	41.5	2335	4	US-10-369-493-2561	Sequence 2561, Ap	232	38	40.4	1734	6	US-11-193-715-6	Sequence 6, Appl
160	39	41.5	2335	5	US-10-732-923-13987	Sequence 13987, A	233	38	40.4	1734	6	US-11-192-967-6	Sequence 6, Appl
161	39.5	41.0	18	5	US-10-782-728-4	Sequence 4, Appl	234	38	40.4	1734	6	US-11-082-454-6	Sequence 6, Appl
162	38.5	41.0	350	3	US-09-764-875-635	Sequence 635, App	235	38	40.4	1753	6	US-11-082-454-6	Sequence 6, Appl
163	38.5	41.0	489	6	US-11-188-298-12374	Sequence 12374, A	236	38	40.4	1791	4	US-10-388-470-42	Sequence 42, Appl
164	38	40.4	51	4	US-10-424-599-170439	Sequence 170439, A	237	38	40.4	1825	5	US-11-082-454-8	Sequence 8, Appl
165	38	40.4	53	4	US-10-424-599-159833	Sequence 159833, A	238	38	40.4	2768	6	US-10-965-017-8	Sequence 8, Appl
166	38	40.4	54	4	US-10-424-599-167213	Sequence 167213, A	239	38	40.4	2787	5	US-10-965-017-2	Sequence 2, Appl
167	38	40.4	59	4	US-10-424-599-274925	Sequence 274925, A	240	38	40.4	93	4	US-10-080-170-425	Sequence 425, App
168	38	40.4	61	4	US-10-437-963-172188	Sequence 172188, A	241	37.5	39.9	93	4	US-10-080-170-425	Sequence 425, App
169	38	40.4	62	4	US-10-424-599-265218	Sequence 265218, A	242	37.5	39.9	93	4	US-10-468-356-425	Sequence 425, App
170	38	40.4	66	4	US-10-424-599-240344	Sequence 240344, A	243	37.5	39.9	111	4	US-10-437-963-105293	Sequence 105293,
171	38	40.4	75	4	US-10-424-599-273038	Sequence 273038, A	244	37.5	39.9	114	5	US-10-745-586-168	Sequence 168, App
172	38	40.4	77	4	US-10-424-599-245224	Sequence 245224, A	245	37.5	39.9	121	4	US-10-437-963-203732	Sequence 203732,
173	38	40.4	86	4	US-10-424-599-230480	Sequence 230480, A	246	37.5	39.9				

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:30:14 ; Search time 118.56 Seconds
(without alignments)
74.233 Million cell updates/sec

Title: US-10-797-626-2

Perfect score: 94

Sequence: 1 KGCSTQNAQLLSLIVGKA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : Published Applications_AA Main:*

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- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	46	48.9	46	4	US-10-437-963-145148
5	46	48.9	274	4	US-10-425-115-187606
6	44.5	47.3	798	4	US-10-437-963-141367
7	44	46.8	347	4	US-10-308-762-240
8	43.5	46.3	606	4	US-10-437-963-106462
9	43	45.7	13	5	US-10-797-626-1
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11	43	45.7	260	3	US-09-989-903-55
12	43	45.7	260	4	US-10-068-564-55
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14	43	45.7	449	6	US-11-097-143-42606
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18	43	45.7	751	6	US-11-114-906-8
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20	43	45.7	764	4	US-10-413-437-6
21	43	45.7	764	6	US-11-114-906-6
22	43	45.7	776	4	US-10-020-079-24
23	43	45.7	776	4	US-10-413-437-24
24	43	45.7	776	6	US-11-114-906-24
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26	43	45.7	789	4	US-10-413-437-22
27	43	45.7	789	6	US-11-114-906-22

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29	43	45.7	838	4	US-10-413-437-40	Sequence 40, Appl
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31	43	45.7	851	4	US-10-020-079-38	Sequence 38, Appl
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33	43	45.7	851	6	US-11-114-906-38	Sequence 38, Appl
34	43	45.7	863	4	US-10-020-079-32	Sequence 32, Appl
35	43	45.7	863	4	US-10-413-437-32	Sequence 32, Appl
36	43	45.7	863	6	US-11-114-906-32	Sequence 32, Appl
37	43	45.7	864	4	US-10-020-079-4	Sequence 4, Appl
38	43	45.7	864	4	US-10-413-437-4	Sequence 4, Appl
39	43	45.7	864	6	US-11-114-906-4	Sequence 4, Appl
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64	43	45.7	1270	4	US-10-408-765A-2253	Sequence 2253, Ap
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66	43	45.7	1321	4	US-10-271-507-2	Sequence 2, Appli
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68	42	44.7	330	5	US-10-450-763-39965	Sequence 39965, A
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97	40	42.6	448	4	US-10-425-115-187601	Sequence 187601, A
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105	36	42.4	1053	2	T30937	probable glycolipi	178	35	41.2	829	1	A33166	colorectal tumor s
106	36	42.4	1118	2	S57833	transmembrane prot	179	35	41.2	862	2	S53913	FKH2 protein - yea
107	36	42.4	1206	2	T43376	DNA-directed RNA p	180	35	41.2	865	1	D70986	probable ABC trans
108	36	42.4	1258	2	T40737	probable calcium-t	181	35	41.2	871	2	A53429	acetylglutamate ki
109	36	42.4	1541	2	AG2474	heterocyst glycoli	182	35	41.2	907	2	H82261	hemolysin-related
110	36	42.4	1765	2	T42714	ankyrin 3, splice	183	35	41.2	1052	2	A56678	yemanuclein-alpha
111	36	42.4	1940	2	T42715	ankyrin 3, splice	184	35	41.2	1078	2	S48842	DNA-directed RNA p
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113	36	42.4	1961	2	T42716	ankyrin 3, splice	186	35	41.2	1196	2	S35994	DNA repair protein
114	36	42.4	2167	2	S19444	hypothetical prote	187	35	41.2	1422	2	T18363	DNA-directed RNA p
115	36	42.4	2225	1	A23443	pyrimidine-synthes	188	35	41.2	1469	2	H96622	probable ABC trans
116	36	42.4	2377	2	A55575	ankyrin 3, long sp	189	35	41.2	1530	2	AH1396	peptidoglycan anch
117	35.5	41.8	496	2	T19027	probable sterol O-	190	35	41.2	2054	2	T07584	hypothetical prote
118	35.5	41.8	614	2	A82832	protein-export mem	191	35	41.2	2155	2	AD2742	conserved hypoteth
119	35	41.2	45	2	PC1154	tumor rejection an	192	35	41.2	2155	2	C75523	hypothetical prote
120	35	41.2	89	2	A87004	probable transcrip	193	35	41.2	2242	2	A57541	pyrimidine synthe
121	35	41.2	99	2	C64489	hypothetical prote	194	35	41.2	4644	1	A38905	dysin heavy chain
122	35	41.2	116	2	E86633	hypothetical prote	195	34.5	40.6	177	2	T23603	hypothetical prote
123	35	41.2	127	2	G87731	protein W10C8.3 li	196	34.5	40.6	449	2	S76839	hypothetical prote
124	35	41.2	137	2	F95996	hypothetical prote	197	34.5	40.6	509	2	A13300	sugar transport AT
125	35	41.2	171	2	S20947	BTG1 protein - hum	198	34.5	40.6	605	2	AF1917	hypothetical prote
126	35	41.2	180	2	G71696	hypothetical prote	199	34.5	40.6	759	2	D84301	cell division cycl
127	35	41.2	181	2	G71696	hypothetical prote	200	34	40.0	49	2	A82039	hypothetical prote
128	35	41.2	184	2	B82307	16S rRNA processin	201	34	40.0	65	2	S02188	hypothetical prote
129	35	41.2	199	2	F71462	hypothetical prote	202	34	40.0	87	2	S33906	probable transcrip
130	35	41.2	245	2	G87066	hypothetical prote	203	34	40.0	87	2	S20912	regulatory protein
131	35	41.2	247	2	T45250	probable phosphori	204	34	40.0	87	2	S29614	whiB protein - Str
132	35	41.2	256	2	A81354	glutamine-binding	205	34	40.0	114	2	D86794	hypothetical prote
133	35	41.2	269	2	B70124	conserved hypoteth	206	34	40.0	125	2	T05633	hypothetical prote
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138	35	41.2	309	2	A80946	FdhE protein (limpo	211	34	40.0	172	2	AD0505	fimbrial chain (im
139	35	41.2	328	2	J00985	hydroxyproline-ric	212	34	40.0	173	2	S18034	pathogenesis-relat
140	35	41.2	343	2	G71979	probable type II D	213	34	40.0	173	2	S18035	thiamatin-like pro
141	35	41.2	387	2	T27287	hypothetical prote	214	34	40.0	173	2	S18035	thiamatin-like pro
142	35	41.2	397	2	F90411	conserved hypoteth	215	34	40.0	173	2	S18524	probable regulator
143	35	41.2	409	2	C82072	D-3-phosphoglycera	216	34	40.0	176	2	G91246	somatotropin precu
144	35	41.2	410	1	DEECGP	phosphoglycerate d	217	34	40.0	190	2	S04355	interferon, tropho
145	35	41.2	410	2	AD0874	D-3-phosphoglycera	218	34	40.0	195	2	A53746	interferon alpha-I
146	35	41.2	410	2	D85947	D-3-phosphoglycera	219	34	40.0	195	2	A61403	interferon omega -
147	35	41.2	411	2	H91101	D-3-phosphoglycera	220	34	40.0	195	2	I47070	interferon alpha -
148	35	41.2	411	2	AF2320	hypothetical prote	221	34	40.0	195	2	I46397	probable guanylate
149	35	41.2	413	2	AC0112	phosphoglycerate d	222	34	40.0	208	2	C70899	hypothetical prote
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151	35	41.2	430	2	I39727	mannopine biosynth	224	34	40.0	224	2	D72046	CT668 hypotethet
152	35	41.2	461	2	D95083	ABC transporter, A	225	34	40.0	224	2	A86579	hypothetical prote
153	35	41.2	461	2	H97950	hypothetical prote	226	34	40.0	238	2	T18788	hypothetical prote
154	35	41.2	473	2	B84143	Na+/H+ antiporter	227	34	40.0	241	2	D72751	hypothetical prote
155	35	41.2	476	1	JC2318	angiotensin precu	228	34	40.0	251	2	G69076	molibdopterin bios
156	35	41.2	486	2	C86645	Glu-tRNA amidotran	229	34	40.0	256	2	AE0511	FixA protein (limpo
157	35	41.2	498	1	VH1VNA	nucleoprotein - in	230	34	40.0	257	2	F86540	CT254 hypotethet
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159	35	41.2	528	2	S19366	hypothetical prote	232	34	40.0	261	2	AH2298	cobalt transport p
160	35	41.2	536	2	T23419	hypothetical prote	233	34	40.0	275	1	R5KT2	ribosomal protein
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162	35	41.2	536	2	D48665	probable Na+/H+-ex	235	34	40.0	277	2	E75187	probable sugar tra
163	35	41.2	536	2	F90839	hypothetical prote	236	34	40.0	277	2	D71220	nematode resistanc
164	35	41.2	538	2	A83018	probable sodium/hy	237	34	40.0	282	2	T50833	arylamine N-acetyl
165	35	41.2	558	2	B48492	polysaccharide exp	238	34	40.0	290	2	B34585	methylenetetrahydr
166	35	41.2	558	2	I41324	polysaccharide exp	239	34	40.0	292	2	T31325	menaquinone biosyn
167	35	41.2	565	1	C72550	methylmalonyl-CoA	240	34	40.0	292	2	A64592	yyak protein - Bac
168	35	41.2	575	2	C83198	probable acyl-CoA	241	34	40.0	299	2	S66007	probable ABC trans
169	35	41.2	577	2	A30723	probable Na+/H+-ex	242	34	40.0	317	2	A81402	probable integral
170	35	41.2	578	2	B7852	phosphotransferase	243	34	40.0	319	2	A95316	annexin X - fruit
171	35	41.2	589	2	A82504	hypothetical prote	244	34	40.0	321	1	LUFF10	hypothetical prote
172	35	41.2	621	2	T15859	hypothetical prote	245	34	40.0	329	2	T32818	hypothetical prote
173	35	41.2	671	2	A65023	hypothetical prote	246	34	40.0	346	2	G83323	hemin permease UU3
174	35	41.2	694	2	C83826	penicillin-binding	247	34	40.0	348	2	E82896	probable peptidogl
175	35	41.2	696	2	F83886	penicillin-binding	248	34	40.0	352	2	H71474	

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:25:14 ; Search time 21.6 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-797-626-3

Perfect score: 85

Sequence: 1 KGGSTQNAQLSLIVGKA 18

Scoring table:

BLOSUM62

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	41	48.2	298	2	D71543
6	41	48.2	372	1	G70817
7	41	48.2	503	1	VMUT1B
8	41	48.2	2756	2	T30183
9	40	47.1	254	2	H69776
10	40	47.1	260	2	D75404
11	40	47.1	285	2	F84986
12	40	47.1	303	2	G64405
13	40	47.1	351	1	A55962
14	40	47.1	389	2	E90039
15	40	47.1	398	2	T44688
16	40	47.1	445	2	D69869
17	40	47.1	1401	2	T02255
18	39.5	46.5	452	2	JG6507
19	39.5	46.5	2335	2	T40186
20	39	45.9	55	2	B97548
21	39	45.9	139	2	D82296
22	39	45.9	227	2	D83162
23	39	45.9	298	2	C81696
24	39	45.9	326	2	AC2953
25	39	45.9	326	2	B98330
26	39	45.9	425	2	C72744
27	39	45.9	699	2	H87275
28	38.5	45.3	431	2	T16191
29	38	44.7	158	2	S75349

30	38	44.7	197	2	AB2571	hypothetical prote
31	38	44.7	203	2	E75145	lsu ribosomal prot
32	38	44.7	206	2	A71185	probable ribosomal
33	38	44.7	292	2	T14627	hypothetical prote
34	38	44.7	317	2	G72342	L-isaspartate(D-a
35	38	44.7	330	2	E88989	protein C36C5.6 [i
36	38	44.7	375	2	C83884	arabinose operon t
37	38	44.7	581	2	B81909	exodeoxyribonuclea
38	38	44.7	850	2	AE1954	hypothetical prote
39	38	44.7	1168	2	I56985	kalinin B1 - mouse
40	38	44.7	1902	1	B44858	lactocepin (EC 3.4
41	38	44.7	2533	2	T28675	alpha-51D immobili
42	38	44.7	2533	2	T28674	alpha-51D-immobili
43	38	44.7	2543	2	T31687	surface antigen - p
44	37.5	44.1	437	2	AF0667	probable phosphotr
45	37	43.5	76	2	AF2168	hypothetical prote
46	37	43.5	101	2	B75168	2-ketoglutarate fe
47	37	43.5	162	2	F81413	hypothetical prote
48	37	43.5	188	2	T52029	hypothetical prote
49	37	43.5	237	2	B84377	dTMP kinase (EC 2.
50	37	43.5	246	2	T00541	hypothetical prote
51	37	43.5	267	2	S72583	abc1 protein - Myc
52	37	43.5	349	1	JC5490	opsin, pineal glan
53	37	43.5	354	2	T36762	probable membrane
54	37	43.5	403	2	C70815	probable beta-reto
55	37	43.5	425	2	D88115	protein F53C3.11 l
56	37	43.5	446	2	D90238	aspartokinase (akH
57	37	43.5	457	2	S03961	Ig mu chain C regi
58	37	43.5	473	2	A86989	conserved hypotet
59	37	43.5	547	2	T00977	probable pectinest
60	37	43.5	561	2	T11378	NADH2 dehydrogenas
61	37	43.5	702	2	JC7890	fructan beta-fruct
62	37	43.5	1217	2	F97177	alpha-glucosidase
63	37	43.5	1347	2	T02214	ubiquitous TPR mot
64	37	43.5	1451	2	B86286	F9L1.15 protein -
65	37	43.5	1499	2	A85813	glutamate synthase
66	37	43.5	1902	2	S06997	lactocepin (EC 3.4
67	37	43.5	1902	2	B45764	lactocepin (EC 3.4
68	37	43.5	1962	2	A32634	lactocepin (EC 3.4
69	37	43.5	2823	2	F87908	protein T22A3.8 [i
70	37	43.5	2823	2	T21064	hypothetical prote
71	37	43.5	3102	2	T43291	laminin alpha chai
72	36.5	42.9	513	2	AI2555	hypothetical prote
73	36	42.4	150	2	AH0371	probable membrane
74	36	42.4	227	2	E83288	probable ATP-bindi
75	36	42.4	310	2	T01869	hypothetical prote
76	36	42.4	323	2	AB1659	hypothetical prote
77	36	42.4	327	2	AB0888	hypothetical prote
78	36	42.4	341	2	S69802	N-acetyluramoyl-L
79	36	42.4	351	2	D82891	conserved hypotet
80	36	42.4	384	2	D90547	oligopeptide ABC t
81	36	42.4	400	2	S76446	hypothetical prote
82	36	42.4	431	2	AB0410	phosphopyruvate hy
83	36	42.4	432	1	NOEC	phosphopyruvate hy
84	36	42.4	432	2	H85928	enolase [imported]
85	36	42.4	432	2	G91083	enolase [imported]
86	36	42.4	432	2	AC0859	enolase [imported]
87	36	42.4	433	2	E82076	enolase VC2447 [im
88	36	42.4	436	2	E64103	phosphopyruvate hy
89	36	42.4	447	2	C70951	hypothetical prote
90	36	42.4	466	2	T01898	hypothetical prote
91	36	42.4	480	2	H85112	hypothetical prote
92	36	42.4	502	2	AF3223	conserved hypotet
93	36	42.4	506	2	H82991	exopolysphatase
94	36	42.4	507	2	T50054	probable transport
95	36	42.4	533	2	A86433	T518.19 protein -
96	36	42.4	585	2	H83199	phosphotransferase
97	36	42.4	597	1	B55513	hoxX protein - Alc
98	36	42.4	601	2	T11677	probable transcrip
99	36	42.4	667	2	D96923	uncharacterized co
100	36	42.4	708	2	T43109	cytolysin B transp
101	36	42.4	780	2	AE0061	organic solvent to
102	36	42.4	841	2	T14398	S-receptor kinase

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:11:36 ; Search time 189.62 Seconds
(without alignments)
92.687 Million cell updates/sec

Title: US-10-797-626-2

Perfect score: 94

Sequence: 1 KGCSTONAQLLSLIVGKA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	56.4	460	2 Q2W121	MAGSA
2	49	52.1	174	2 Q2S7G9	9GAMM
3	48	51.1	577	2 Q2W64	CLOBE
4	47	50.0	301	1 IAN4	MOUSE
5	47	50.0	301	2 Q4VBX0	MOUSE
6	47	50.0	301	2 Q549W4	MOUSE
7	47	50.0	370	1 SLD1	DICDI
8	46	48.9	99	2 Q2RMN8	RHORU
9	46	48.9	427	2 Q4WKC3	ASPFU
10	46	48.9	523	2 Q3ORZ0	9RHOB
11	46	48.9	684	2 Q4NHR6	9MCC
12	45	47.9	510	2 Q38CP5	9TRYR
13	44.5	47.3	82	2 Q225W6	9GAMM
14	44.5	47.3	82	2 Q35WU8	9GAMM
15	44.5	47.3	798	2 Q6ZD67	ORYSA
16	44	46.8	150	2 Q9L3N1	MICAE
17	44	46.8	165	2 Q87RY4	VIBPA
18	44	46.8	169	2 Q87J15	VIBPA
19	44	46.8	191	2 Q55T15	CRYNE
20	44	46.8	191	2 Q5KIV2	CRYNE
21	44	46.8	285	1 FOLD	BUCAI
22	44	46.8	294	2 Q423F6	DESHA
23	44	46.8	308	2 Q5AYR6	EMENI
24	44	46.8	357	2 Q8SUY1	ENCCU
25	44	46.8	801	2 Q20550	CAEEL
26	44	46.8	865	2 Q3RA20	VIBMA
27	44	46.8	2542	2 Q3QG44	9GAMM
28	43.5	46.3	341	2 Q5NR30	ZYMMO
29	43.5	46.3	606	2 Q5Z619	ORYSA
30	43	45.7	272	2 Q3QUH1	9RHOB
31	43	45.7	287	2 Q9H6N8	HUMAN

32	43	45.7	449	1 CSUP	DROME
33	43	45.7	452	1 CASP2	MOUSE
34	43	45.7	452	1 CASP2	RAT
35	43	45.7	463	2 Q750V4	ASHGO
36	43	45.7	621	2 Q6ZNH0	HUMAN
37	43	45.7	621	2 Q7NIC2	GLOVI
38	43	45.7	782	2 Q3URR7	MOUSE
39	43	45.7	790	2 Q02744	PNECA
40	43	45.7	813	2 Q5WHJ9	BACSK
41	43	45.7	819	2 Q3M6E0	ANAVT
42	43	45.7	883	2 Q8SRT2	ENCCU
43	43	45.7	1320	2 Q96JH2	HUMAN
44	43	45.7	1321	2 Q2L6C6	HUMAN
45	43	45.7	1414	2 Q5TCY1	HUMAN
46	43	45.7	1521	2 Q54X75	DICDI
47	43	45.7	2884	2 Q4SHN1	TETNG
48	43	44.7	71	1 NIFU	PRAAL
49	42	44.7	106	2 Q8R454	MESAU
50	42	44.7	121	2 Q44M14	CHLLI
51	42	44.7	168	2 Q4XMH7	PLACH
52	42	44.7	183	2 Q54X41	DICDI
53	42	44.7	239	2 Q2PYA2	9BACT
54	42	44.7	268	2 Q3AIY2	PELCD
55	42	44.7	276	2 Q4ZVM9	PSEU2
56	42	44.7	294	2 Q4UCD1	THEAN
57	42	44.7	303	1 CD47	BOVIN
58	42	44.7	377	2 Q4U9E7	THEAN
59	42	44.7	424	2 Q3SZH5	BOVIN
60	42	44.7	508	2 Q56V71	9ROSI
61	42	44.7	515	2 Q56VA6	9ROSI
62	42	44.7	599	2 Q8OPH5	CABER
63	42	44.7	675	2 Q8SV89	ENCCU
64	42	44.7	698	2 Q8QKX8	9PHYC
65	42	44.7	719	2 Q3UKU5	MOUSE
66	42	44.7	719	2 Q510Y2	MOUSE
67	42	44.7	733	2 Q7UJB6	RHOBA
68	42	44.7	852	2 Q37R76	SPHAR
69	42	44.7	852	2 Q4T128	TETNG
70	42	44.7	1092	1 LIFR	MOUSE
71	42	44.7	1092	2 Q3U234	MOUSE
72	42	44.7	1731	2 Q72TM8	LEPIC
73	42	44.7	1731	2 Q8FIM0	LEPIN
74	42	44.7	1222	2 Q41XZ0	DESHA
75	41.5	44.1	128	2 Q6LW22	PHOPR
76	41.5	44.1	133	2 Q4APZ0	9CHLB
77	41.5	44.1	859	2 Q61FT5	MOUSE
78	41.5	44.1	860	2 Q61FT6	RAT
79	41	43.6	167	2 Q8TXW4	METKA
80	41	43.6	174	2 Q5KPD8	CRYNE
81	41	43.6	224	2 Q590H3	9PRIM
82	41	43.6	226	2 Q590I1	9PRIM
83	41	43.6	228	2 Q590H7	HUMAN
84	41	43.6	228	2 Q590H2	HYLLA
85	41	43.6	228	2 Q590H4	PREEN
86	41	43.6	228	2 Q590H5	LEORO
87	41	43.6	228	2 Q590H6	CHEME
88	41	43.6	228	2 Q590H8	PONPY
89	41	43.6	228	2 Q590H9	MACFA
90	41	43.6	228	2 Q590I0	ATEGE
91	41	43.6	228	2 Q590I2	LEMCA
92	41	43.6	229	2 Q3G008	9DELT
93	41	43.6	230	2 Q84FK5	ENTAG
94	41	43.6	240	2 Q06170	YEAST
95	41	43.6	260	2 Q4CN69	TRYCR
96	41	43.6	263	1 ONCM	MOUSE
97	41	43.6	263	2 Q3UIY5	MOUSE
98	41	43.6	263	2 Q5SPX6	MOUSE
99	41	43.6	278	2 Q34X74	9GAMM
100	41	43.6	308	2 Q5QSQ6	CRYNE
101	41	43.6	350	2 Q61Z77	CABER
102	41	43.6	427	2 Q9VVQ2	DROME
103	41	43.6	428	1 TERM	DROME
104	41	43.6	428	2 Q541G1	DROME

Q9V3A4	drosophila
P29594	m caspase-2
F55215	rattus norv
Q750V4	ashbya goss
Q6ZNH0	homo sapien
Q7NIC2	gloeobacter
Q3URR7	mus musculus
Q02744	pneumocysti
Q5WHJ9	bacillus cl
Q3M6E0	anabaena va
Q8SRT2	encephalito
Q96JH2	homo sapien
Q2L6C6	homo sapien
Q5TCY1	homo sapien
Q54X75	dictyosteli
Q4SHN1	tetradon n
P46045	frankia aln
Q8R454	mesocricetu
Q44M14	chlorobium
Q4XMH7	plasmodium
Q54X41	dictyosteli
Q2PYA2	uncultured
Q3AIY2	pelobacter
Q4ZVM9	pseudomonas
Q4UCD1	thelateria a
Q9N0K1	bos taurus
Q4U9E7	thelateria a
Q3SZH5	bos taurus
Q56V71	thecacoris
Q56VA6	antidesma a
Q8OPH5	caenorhabdi
Q8SV89	encephalito
Q8QKX8	ectocarpus
Q3UKU5	mus musculus
Q510Y2	mus musculus
Q7UJB6	rhodospirell
Q37R76	novosphingo
Q4T128	tetradon n
P42703	mus musculus
Q3U234	mus musculus
Q72TM8	leptospora
Q8FIM0	leptospora
Q41XZ0	desulfitoba
Q6LW22	photobacter
Q4APZ0	chlorobium
Q61FT5	mus musculus
Q61FT6	rattus norv
Q8TXW4	methanopyru
Q5KPD8	cryptococcu
Q590H3	colobus sp.
Q590I1	gorilla gor
Q590H7	homo sapien
Q590H2	hylobates l
Q590H4	presbytis e
Q590H5	leontopithe
Q590H6	cheirogaleu
Q590H8	pongo pygma
Q590H9	ataca fasc
Q590I0	ateles geof
Q590I2	lemur catta
Q3G008	pelobacter
Q84FK5	enterobacte
Q06170	saccharomyc
Q4CN69	trypanosoma
P53347	mus musculus
Q3UIY5	mus musculus
Q5SPX6	mus musculus
Q34X74	alkalilimni
Q5QSQ6	cryptococcu
Q61Z77	caenorhabdi
Q9VVQ2	drosophila
P11455	drosophila
Q541G1	drosophila

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:11:36 ; Search time 179.64 Seconds
(without alignments)
92.687 Million cell updates/sec

Title: US-10-797-626-3

Perfect score: 85
Sequence: 1 KGGSTQNAQLLSLVGKA 18

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	58.8	174	2	Q2S7G9_9GAMM
2	46	54.1	99	2	Q2RMN8_RHODU
3	46	54.1	329	2	Q44LV6_CHLIL
4	46	54.1	883	2	QASRT2_ENCCU
5	45.5	53.5	698	2	Q8QKX8_PHYC
6	45	52.9	261	2	Q9G9I8_OCHDN
7	45	52.9	798	2	Q6ZD67_ORYSA
8	45	52.9	819	2	Q3M6E0_ANAVT
9	44	51.8	148	1	NRDI_CORGL
10	44	51.8	201	1	RL18_PYRKO
11	44	51.8	260	2	Q4CN69_TRYCR
12	44	51.8	391	2	Q974X7_SULTO
13	44	51.8	627	2	Q4E2E3_TRYCR
14	44	51.8	2542	2	Q3QG44_9GAMM
15	43	50.6	83	2	Q8EDD9_SHEON
16	43	50.6	296	2	Q9Z8S5_CHLPN
17	43	50.6	297	2	Q823A8_CHLCV
18	43	50.6	321	2	Q58GZ9_9NEOP
19	43	50.6	321	2	Q58H36_9NEOP
20	43	50.6	321	2	Q58H42_9NEOP
21	43	50.6	321	2	Q58GZ1_9NEOP
22	43	50.6	331	2	Q58GZ5_9NEOP
23	43	50.6	331	2	Q58GZ6_9NEOP
24	43	50.6	331	2	Q58H16_9NEOP
25	43	50.6	331	2	Q58H17_9NEOP
26	43	50.6	331	2	Q58H21_9NEOP
27	43	50.6	331	2	Q58H31_9NEOP
28	43	50.6	331	2	Q4NLB8_9MCC
29	43	50.6	334	2	Q6TUE9_RAT
30	43	50.6	340	2	Q58H24_9NEOP
31	43	50.6	340	2	Q58H44_9NEOP

32	43	50.6	350	2	Q58GY8_9NEOP
33	43	50.6	350	2	Q58GZ3_9NEOP
34	43	50.6	350	2	Q58H01_9NEOP
35	43	50.6	350	2	Q58H02_9NEOP
36	43	50.6	350	2	Q58H03_9NEOP
37	43	50.6	350	2	Q58H06_9NEOP
38	43	50.6	350	2	Q58H07_9NEOP
39	43	50.6	350	2	Q58H08_9NEOP
40	43	50.6	350	2	Q58H12_9NEOP
41	43	50.6	350	2	Q58H18_9NEOP
42	43	50.6	350	2	Q58H19_9NEOP
43	43	50.6	350	2	Q58H23_9NEOP
44	43	50.6	350	2	Q58H50_9NEOP
45	43	50.6	476	2	Q95YG8_PSESE
46	43	50.6	476	2	Q95YG9_MAMBR
47	43	50.6	643	2	Q8YSE2_ANASP
48	43	50.6	850	2	Q55UC0_CRYNE
49	43	50.6	850	2	Q5KI25_CRYNE
50	43	50.6	936	2	Q3GC24_9FIRM
51	43	50.6	1861	2	Q5CZH9_HUMAN
52	42.5	50.0	991	2	Q4IQZ5_GIBZE
53	42	49.4	308	2	Q5AYR6_EMBE1
54	42	49.4	349	2	Q4TGT6_TETNG
55	42	49.4	353	2	Q4I5V6_GIBZE
56	42	49.4	356	2	Q4SUT8_TETNG
57	42	49.4	413	2	Q4QOE5_SCHMA
58	42	49.4	508	2	Q56V71_9ROSI
59	42	49.4	515	2	Q56VA6_9ROSI
60	42	49.4	531	2	Q97HQ2_CLOAB
61	42	49.4	553	1	FNS1_KLUJLA
62	42	49.4	587	2	Q4Z9F2_9CAUD
63	42	49.4	787	2	Q55DT6_DICD1
64	42	49.4	872	2	Q5SRQ8_CRYNE
65	42	49.4	872	2	Q5KG63_CRYNE
66	41	48.2	292	2	Q3VB26_9SPHN
67	41	48.2	297	2	Q5L5X4_CHLAB
68	41	48.2	298	2	Q3KME1_CHLTA
69	41	48.2	336	2	Q7X2Z2_CHLTR
70	41	48.2	336	2	Q7X2Z2_9BACT
71	41	48.2	350	2	Q61Z77_CAEER
72	41	48.2	372	2	Q53916_MYCTU
73	41	48.2	503	1	VSA1_TRYBB
74	41	48.2	512	2	Q3K7I3_PSEPF
75	41	48.2	522	2	Q3ADH2_CARHZ
76	41	48.2	523	2	Q9FDZ1_ORYSA
77	41	48.2	577	2	Q2WM64_CLOBE
78	41	48.2	589	2	Q8ETK3_OCEIH
79	41	48.2	591	2	Q8VJZ4_MYCTU
80	41	48.2	591	2	Q7TZU2_MYCBO
81	41	48.2	633	2	Q7X188_ORYSA
82	41	48.2	638	2	Q43ZL5_SOLUS
83	41	48.2	848	2	Q3M5K6_ANAVT
84	41	48.2	996	2	Q3QNM4_GEONG
85	41	48.2	1399	1	RPOC_PSE14
86	41	48.2	1399	1	RPOC_PSESM
87	41	48.2	1399	1	RPOC_PSEU2
88	41	48.2	2664	2	Q3P4K1_9GAMM
89	41	48.2	2756	2	Q33904_9GAMM
90	41	48.2	3211	2	Q4KJ19_PSEF5
91	40.5	47.6	483	2	Q3OB58_ACIG3
92	40	47.1	66	2	Q8MXH4_CAEEL
93	40	47.1	201	2	Q7O6Z3_ANOGA
94	40	47.1	224	2	Q590H3_9PRIM
95	40	47.1	226	2	Q590I1_9PRIM
96	40	47.1	228	2	Q392N2_GEONG
97	40	47.1	228	2	Q590H7_HUMAN
98	40	47.1	228	2	Q590H2_HYLLA
99	40	47.1	228	2	Q590H4_PREEN
100	40	47.1	228	2	Q590H5_LEORO
101	40	47.1	228	2	Q590H6_CHEME
102	40	47.1	228	2	Q590H8_PONPY
103	40	47.1	228	2	Q590H9_MACFA
104	40	47.1	228	2	Q590I0_ATEGE

105	40	47.1	228	2	Q59012	lemur catta	Q59012	178	39.5	46.5	452	1	CASP2_RAT	P55215	rattus norv
106	40	47.1	254	2	P96655	BACSU	P96655	179	39.5	46.5	2335	1	TOR1_SCHPO	O14356	schizosacch
107	40	47.1	260	2	Q9RUM9	DEIRA	Q9RUM9	180	39.5	46.5	3966	1	Q7KVA7_DROME	Q7KVA7	drosophila
108	40	47.1	285	1	FOLD_BUCAI		P57557	181	39	45.9	55	2	Q8USA6_AGR5	Q8USA6	agrobacteri
109	40	47.1	285	2	Q8XW1_CLOPE		Q8XW1	182	39	45.9	139	2	Q9KU74_VIBCH	Q9KU74	vibrio chol
110	40	47.1	286	2	Q4MMH9_BACCE		Q4MMH9	183	39	45.9	144	2	Q8ZIQ5_PYRAE	Q8ZIQ5	pyrobaculum
111	40	47.1	286	2	Q63CM0_BACCCZ		Q63CM0	184	39	45.9	170	2	Q4C517_CROWT	Q4C517	crocosphaer
112	40	47.1	286	2	Q6HK25_BACHCZ		Q6HK25	185	39	45.9	189	2	Q3ZYJ7_DEHSC	Q3ZYJ7	dehalococco
113	40	47.1	286	2	Q81EN8_BACCR		Q81EN8	186	39	45.9	198	2	Q8B990_SHEON	Q8B990	shewanella
114	40	47.1	286	2	Q81RV2_BACAN		Q81RV2	187	39	45.9	198	2	Q5QF97_9CRUS	Q5QF97	amblyops ab
115	40	47.1	286	2	Q739X4_BACCI		Q739X4	188	39	45.9	213	2	Q8GVF4_ORISA	Q8GVF4	oryza sativ
116	40	47.1	289	2	Q4VOK7_BACTI		Q4VOK7	189	39	45.9	225	2	Q41QS9_FERAC	Q41QS9	ferroplasma
117	40	47.1	293	2	Q3EWR3_BACTI		Q3EWR3	190	39	45.9	225	2	Q3XM71_9PROT	Q3XM71	magnetococc
118	40	47.1	293	2	Q8PEA8_XANCP		Q8PEA8	191	39	45.9	226	2	Q590H1_ATEGE	Q590H1	ateles geof
119	40	47.1	303	1	MYRE_METJA		Q58257	192	39	45.9	226	2	Q9FOX4_PSEFL	Q9FOX4	pseudomonas
120	40	47.1	318	2	Q7MAC8_WOLSU		Q7MAC8	193	39	45.9	227	2	Q54046_PSEAE	Q54046	pseudomonas
121	40	47.1	351	1	Q8SP_CHICK		P51475	194	39	45.9	232	2	Q7U5L5_SYNFX	Q7U5L5	synecococc
122	40	47.1	358	2	Q5JGK9_PYRKO		Q5JGK9	195	39	45.9	251	2	Q5P7N8_AZOSE	Q5P7N8	azarococcus sp
123	40	47.1	378	2	Q364K2_DROBS		Q364K2	196	39	45.9	268	2	Q3AIY2_PELCD	Q3AIY2	pelobacter
124	40	47.1	384	2	Q6KY77_PICTO		Q6KY77	197	39	45.9	278	2	Q34X74_9GAMM	Q34X74	alkalilimni
125	40	47.1	385	2	Q4L805_STAHI		Q4L805	198	39	45.9	286	2	Q31TE1_SHIBS	Q31TE1	shigella bo
126	40	47.1	389	2	Q2YZ45_STAAB		Q2YZ45	199	39	45.9	286	2	Q3YUD5_SHISS	Q3YUD5	shigella so
127	40	47.1	389	2	Q6G6T3_STAAS		Q6G6T3	200	39	45.9	298	2	Q9PKH1_CHLMU	Q9PKH1	chlamydia m
128	40	47.1	389	2	Q7A3U8_STAAR		Q7A3U8	201	39	45.9	314	1	RT09_NEUCR	RT09	neurospora
129	40	47.1	389	2	Q8NV31_STAAN		Q8NV31	202	39	45.9	323	2	Q36TT7_MARHY	Q36TT7	marinobacte
130	40	47.1	389	2	Q39RP1_STAAM		Q39RP1	203	39	45.9	326	2	Q89QC5_BRAJA	Q89QC5	bradyrhizob
131	40	47.1	389	2	Q8NDV7_TYCR		Q8NDV7	204	39	45.9	326	2	Q8UAZ2_AGR5	Q8UAZ2	agrobacteri
132	40	47.1	389	2	Q8HDG7_STAAC		Q8HDG7	205	39	45.9	340	2	Q58H22_9NEOP	Q58H22	micrathetis
133	40	47.1	396	2	Q3MZK3_9DEL		Q3MZK3	206	39	45.9	350	2	Q58H43_9NEOP	Q58H43	autographa
134	40	47.1	398	2	Q87694_BACME		Q87694	207	39	45.9	383	2	Q5W9U0_RHIOR	Q5W9U0	rhizopus or
135	40	47.1	409	2	Q4T9R3_TETNG		Q4T9R3	208	39	45.9	425	2	Q5YEU9_AERPE	Q5YEU9	aeropyrum p
136	40	47.1	419	2	Q4D193_TYCR		Q4D193	209	39	45.9	452	2	Q5V618_HALMA	Q5V618	haloarcula
137	40	47.1	419	2	Q4DNV8_TYCR		Q4DNV8	210	39	45.9	459	2	Q4WV68_ASPFU	Q4WV68	aspergillus
138	40	47.1	435	2	Q5AAL8_CNAL		Q5AAL8	211	39	45.9	465	2	Q4B7K1_BURVI	Q4B7K1	burkholderi
139	40	47.1	445	1	YKVU_BACSU		Q5A168	212	39	45.9	467	2	Q7SX10_BRARE	Q7SX10	brachydanio
140	40	47.1	446	2	Q2SK37_9GAMM		Q2SK37	213	39	45.9	481	2	Q6SPX9_MANSM	Q6SPX9	mannheimia
141	40	47.1	475	2	Q5W6J8_ORISA		Q5W6J8	214	39	45.9	508	2	Q4VWM2_2ROSI	Q4VWM2	hymenocardi
142	40	47.1	501	2	Q622W8_CAEBR		Q622W8	215	39	45.9	524	2	Q21LGO_BORAV	Q21LGO	bordetella
143	40	47.1	503	2	Q4DNV7_TYCR		Q4DNV7	216	39	45.9	529	2	Q21696_CAEL	Q21696	caenorhabdi
144	40	47.1	503	2	Q5PK9_TYCR		Q5PK9	217	39	45.9	582	2	Q9V4W9_DROME	Q9V4W9	drosophila
145	40	47.1	508	2	Q56V70_9ROSI		Q56V70	218	39	45.9	617	2	Q2W986_MAGSA	Q2W986	magnetospor
146	40	47.1	588	2	Q4D192_TYCR		Q4D192	219	39	45.9	619	1	EX070_KLULA	EX070	kluyveromyc
147	40	47.1	608	2	Q4NIP7_9MICC		Q4NIP7	220	39	45.9	619	2	Q617F9_CAEBR	Q617F9	caenorhabdi
148	40	47.1	611	2	Q2WPN6_CLOPE		Q2WPN6	221	39	45.9	632	2	Q7XMF5_ORISA	Q7XMF5	oryza sativ
149	40	47.1	636	2	Q3ZL21_ESCBL		Q3ZL21	222	39	45.9	641	2	Q8ZWQ5_PYRAE	Q8ZWQ5	pyrobaculum
150	40	47.1	670	2	Q8ZTL6_PYRAE		Q8ZTL6	223	39	45.9	670	2	Q9W474_DROME	Q9W474	drosophila
151	40	47.1	798	2	Q6ZC60_ORISA		Q6ZC60	224	39	45.9	699	2	Q9ABL0_CAUCR	Q9ABL0	caulobacter
152	40	47.1	996	2	Q8R2W5_MOUSE		Q8R2W5	225	39	45.9	705	2	Q6AX28_XENLA	Q6AX28	xenopus lae
153	40	47.1	1007	2	Q4AS60_9BURK		Q4AS60	226	39	45.9	716	2	Q2PGX3_9PERC	Q2PGX3	takifugu ob
154	40	47.1	1025	2	Q4OS18_DESAC		Q4OS18	227	39	45.9	721	2	Q4CSH4_TYCR	Q4CSH4	trypanosoma
155	40	47.1	1035	2	Q86TD1_HUMAN		Q86TD1	228	39	45.9	721	2	Q4DDA0_TYCR	Q4DDA0	trypanosoma
156	40	47.1	1150	2	Q6D180_MOUSE		Q6D180	229	39	45.9	810	2	Q3SEM6_PARTE	Q3SEM6	paramecium
157	40	47.1	1206	2	Q8ZXP1_PYRAE		Q8ZXP1	230	39	45.9	866	2	Q4SHZ0_TETNG	Q4SHZ0	tetradion n
158	40	47.1	1333	1	UTX_MOUSE		Q70546	231	39	45.9	1040	2	Q54U93_DICDI	Q54U93	dictyosteli
159	40	47.1	1401	1	UTX_HUMAN		Q15550	232	39	45.9	1112	2	Q8GD29_BORAV	Q8GD29	bordetella
160	40	47.1	1401	2	Q52L19_HUMAN		Q52L19	233	39	45.9	1219	2	Q21L04_BORAV	Q21L04	bordetella
161	40	47.1	1401	2	Q5JV43_HUMAN		Q5JV43	234	39	45.9	1239	2	Q9FBZ4_SIRCO	Q9FBZ4	streptomyce
162	40	47.1	1406	2	Q59HG3_HUMAN		Q59HG3	235	39	45.9	1390	2	Q54U91_DICDI	Q54U91	dictyosteli
163	40	47.1	1424	2	Q7TSG4_MOUSE		Q7TSG4	236	39	45.9	1485	2	Q2R0G9_ORISA	Q2R0G9	oryza sativ
164	40	47.1	1455	2	Q6AZS3_XENLA		Q6AZS3	237	39	45.9	1513	2	Q4ASQ1_CHICH	Q4ASQ1	chlostridium
165	40	47.1	2122	2	Q41X20_DESHA		Q41X20	238	39	45.9	1943	2	Q4KKQ1_SCHMA	Q4KKQ1	schistosoma
166	40	47.1	2531	2	Q8EGK0_SHEON		Q8EGK0	239	39	45.9	2405	2	Q3NUK2_SHEFLA	Q3NUK2	shewanella
167	40	47.1	2573	2	Q3CG8_PHOPR		Q3CG8	240	39	45.9	3620	2	Q32ZD3_9FLAV	Q32ZD3	sepiak virus
168	40	47.1	2581	2	Q6LS55_PHOPR		Q6LS55	241	39	45.9	4236	2	Q5U9X1_TERTH	Q5U9X1	tetrahymena
169	40	47.1	2619	2	Q33TP3_9GAMM		Q33TP3	242	38.5	45.3	270	2	Q2N7F8_9SPHN	Q2N7F8	erythroba
170	40	47.1	2624	2	Q368M8_9GAMM		Q368M8	243	38.5	45.3	341	2	Q3QUH1_9RHO	Q3QUH1	silicibacte
171	40	47.1	2640	2	Q35Z06_9GAMM		Q35Z06	244	38.5	45.3	341	2	Q5NR30_ZYMO	Q5NR30	zymomonas m
172	40	47.1	2642	2	Q3ZRO9_SHEPU		Q3ZRO9	245	38.5	45.3	416	2	Q2WI29_CLOBE	Q2WI29	clostridium
173	40	47.1	2644	2	Q2X787_9GAMM		Q2X787	246	38.5	45.3	513	2	Q19846_CAEL	Q19846	caenorhabdi
174	40	47.1	2657	2	Q3Z774_9GAMM		Q3Z774	247	38.5	45.3	513	2	Q612F1_CAEBL	Q612F1	caenorhabdi
175	40	47.1	2693	2	Q3Q6R8_9GAMM		Q3Q6R8	248	38.5	45.3	515	2	Q5WRR6_CAEBL	Q5WRR6	caenorhabdi
176	40	47.1	6274	2	Q880E1_PSESM		Q880E1	249	38.5	45.3	893	2	O12274_simian t-ly	O12274	simian t-ly
177	39.5	46.5	452	1	CASP2_MOUSE		P29594	250	38.5	45.3	893	2	Q6XQ04_9DELA	Q6XQ04	simian t-ly

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:29:13 ; Search time 33.48 Seconds
(without alignments)
47.059 Million cell updates/sec

Title: US-10-797-626-3

Perfect score: 85

Sequence: 1 KGGSTQNAQLLSLVGKA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents_AA*

1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB pep.*

2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB pep.*

3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB pep.*

4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB pep.*

5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCITUS COMB pep.*

6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB pep.*

7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	50.6	313	2	US-09-198-452A-275 Sequence 275, App
2	43	50.6	321	2	US-09-438-185A-265 Sequence 265, App
3	41	48.2	151	1	US-08-253-155A-44 Sequence 44, Appl
4	41	48.2	2756	1	US-08-375-709-11 Sequence 11, Appl
5	41	48.2	2756	1	US-08-752-929-11 Sequence 11, Appl
6	41	48.2	2756	2	US-09-090-793-7 Sequence 7, Appl
7	41	48.2	2756	2	US-09-231-899-7 Sequence 7, Appl
8	40.5	47.6	696	2	US-09-489-039A-12404 Sequence 12404, A
9	40	47.1	201	2	US-09-248-796A-19314 Sequence 19314, A
10	40	47.1	371	2	US-09-252-991A-29955 Sequence 29955, A
11	40	47.1	1401	2	US-09-976-594-1035 Sequence 1035, App
12	39.5	46.5	260	2	US-09-187-789-55 Sequence 55, Appl
13	39.5	46.5	260	2	US-09-139-600-50 Sequence 50, Appl
14	39.5	46.5	260	2	US-09-989-903-55 Sequence 55, Appl
15	39	45.9	485	2	US-09-252-991A-20388 Sequence 20388, A
16	38	44.7	54	2	US-09-583-110-4339 Sequence 4339, App
17	38	44.7	63	2	US-09-107-433-4770 Sequence 4770, App
18	38	44.7	154	2	US-09-489-039A-11527 Sequence 11527, A
19	38	44.7	285	2	US-09-543-681A-7202 Sequence 7202, App
20	38	44.7	324	2	US-09-252-991A-29070 Sequence 29070, A
21	38	44.7	550	2	US-09-489-039A-13969 Sequence 13969, A
22	38	44.7	645	2	US-09-710-279-2984 Sequence 2984, App
23	38	44.7	1005	2	US-09-134-000C-6322 Sequence 6322, App
24	38	44.7	1501	2	US-09-710-279-2850 Sequence 2850, App
25	38	44.7	1529	2	US-09-134-001C-3945 Sequence 3945, App
26	37	43.5	76	2	US-09-270-767-34207 Sequence 34207, A

27	37	43.5	76	2	US-09-270-767-49424 Sequence 49424, A
28	37	43.5	282	2	US-09-107-532A-5553 Sequence 5553, App
29	37	43.5	441	2	US-09-950-071-2 Sequence 2, Appl
30	37	43.5	612	1	US-08-746-283-31 Sequence 31, Appl
31	37	43.5	612	1	US-08-746-257A-29 Sequence 29, Appl
32	37	43.5	613	1	US-08-746-283-1 Sequence 1, Appl
33	37	43.5	613	1	US-08-746-283-3 Sequence 3, Appl
34	37	43.5	613	1	US-08-746-283-5 Sequence 5, Appl
35	37	43.5	613	1	US-08-746-257A-1 Sequence 1, Appl
36	37	43.5	613	2	US-09-347-878-48 Sequence 48, Appl
37	37	43.5	896	2	US-09-543-681A-5439 Sequence 5439, App
38	37	43.5	1079	2	US-09-058-489-22 Sequence 22, Appl
39	37	43.5	1240	2	US-09-058-489-23 Sequence 23, Appl
40	37	43.5	1347	2	US-09-058-489-24 Sequence 24, Appl
41	36.5	42.9	306	2	US-09-107-532A-5918 Sequence 5918, App
42	36.5	42.9	3174	1	US-08-477-451-3 Sequence 3, Appl
43	36	42.4	71	2	US-09-248-796A-23149 Sequence 23149, A
44	36	42.4	214	2	US-09-198-452A-75 Sequence 75, Appl
45	36	42.4	240	2	US-09-252-991A-17600 Sequence 17600, A
46	36	42.4	257	2	US-09-252-991A-27607 Sequence 27607, A
47	36	42.4	285	2	US-09-252-991A-26081 Sequence 26081, A
48	36	42.4	290	2	US-09-543-681A-6981 Sequence 6981, App
49	36	42.4	297	2	US-09-134-000C-4187 Sequence 4187, App
50	36	42.4	348	2	US-09-134-000C-5396 Sequence 5396, App
51	36	42.4	355	2	US-10-104-047-3556 Sequence 3556, App
52	36	42.4	394	2	US-09-107-532A-5184 Sequence 5184, App
53	36	42.4	456	2	US-09-543-681A-6090 Sequence 6090, App
54	36	42.4	459	2	US-09-489-039A-10061 Sequence 10061, A
55	36	42.4	506	2	US-09-949-016-7018 Sequence 7018, App
56	36	42.4	516	2	US-09-949-016-7989 Sequence 7989, App
57	36	42.4	557	2	US-09-252-991A-22750 Sequence 22750, A
58	36	42.4	657	2	US-09-543-681A-7109 Sequence 7109, App
59	36	42.4	771	2	US-09-634-238-229 Sequence 229, App
60	36	42.4	771	2	US-09-634-238-262 Sequence 262, App
61	36	42.4	780	2	US-09-785-381-11 Sequence 11, Appl
62	36	42.4	1088	2	US-09-082-059-2 Sequence 2, Appl
63	36	42.4	1287	2	US-09-252-991A-29606 Sequence 29606, A
64	36	42.4	1724	2	US-09-964-899-43 Sequence 43, Appl
65	36	42.4	3913	2	US-09-949-016-10933 Sequence 10933, A
66	36	42.4	4377	2	US-09-949-016-6978 Sequence 6978, App
67	35.5	41.8	496	2	US-09-326-203A-18 Sequence 18, Appl
68	35	41.2	20	2	US-09-962-756-1190 Sequence 1190, App
69	35	41.2	21	2	US-09-962-756-1649 Sequence 1649, App
70	35	41.2	85	2	US-09-270-767-59587 Sequence 59587, A
71	35	41.2	87	2	US-09-605-703B-1868 Sequence 1868, App
72	35	41.2	171	2	US-08-718-738-17 Sequence 17, Appl
73	35	41.2	171	2	US-09-221-844-17 Sequence 17, Appl
74	35	41.2	171	2	US-09-843-846-17 Sequence 17, Appl
75	35	41.2	210	2	US-09-489-039A-8681 Sequence 8681, App
76	35	41.2	212	2	US-09-270-767-59436 Sequence 59436, A
77	35	41.2	221	2	US-09-949-016-7387 Sequence 7387, App
78	35	41.2	231	2	US-09-134-000C-6021 Sequence 6021, App
79	35	41.2	248	2	US-09-634-238-279 Sequence 279, App
80	35	41.2	249	2	US-08-591-468-2 Sequence 2, Appl
81	35	41.2	249	2	US-09-605-703B-1920 Sequence 38, Appl
82	35	41.2	249	2	US-09-650-324A-38 Sequence 38, Appl
83	35	41.2	249	5	PCT-US94-06430-38 Sequence 2, Appl
84	35	41.2	273	2	US-08-928-213B-9 Sequence 9, Appl
85	35	41.2	276	2	US-09-605-703B-1920 Sequence 1920, App
86	35	41.2	288	2	US-09-489-039A-8919 Sequence 8919, App
87	35	41.2	289	2	US-09-716-964B-26 Sequence 26, Appl
88	35	41.2	292	2	US-08-858-207A-391 Sequence 391, App
89	35	41.2	292	2	US-09-583-110-3607 Sequence 3607, App
90	35	41.2	302	2	US-09-107-433-4911 Sequence 4911, App
91	35	41.2	309	2	US-09-489-039A-12224 Sequence 12224, A
92	35	41.2	312	2	US-09-134-001C-3534 Sequence 3534, App
93	35	41.2	312	2	US-09-710-279-3104 Sequence 3104, App
94	35	41.2	316	2	US-09-252-991A-21365 Sequence 21365, A
95	35	41.2	318	2	US-09-270-767-44026 Sequence 44026, A
96	35	41.2	348	2	US-09-270-767-44163 Sequence 44163, A
97	35	41.2	375	2	US-09-444-412-2 Sequence 2, Appl
98	35	41.2	375	2	US-09-660-742-12 Sequence 12, Appl
99	35	41.2	375	2	US-09-825-414-36 Sequence 36, Appl

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100	35	41.2	375	2	US-09-825-414-62	Sequence 62, Appl	173	34	40.0	102	1	US-08-455-524B-26	Sequence 26, Appl
101	35	41.2	391	2	US-09-347-798-8	Sequence 8, Appl	174	34	40.0	102	1	US-08-455-021B-26	Sequence 26, Appl
102	35	41.2	410	2	US-08-411-760-14	Sequence 14, Appl	175	34	40.0	102	1	US-09-045-467-26	Sequence 26, Appl
103	35	41.2	412	2	US-09-540-236-3010	Sequence 3010, Ap	176	34	40.0	115	2	US-09-471-276-1439	Sequence 1439, Ap
104	35	41.2	415	2	US-09-347-798-10	Sequence 10, Appl	177	34	40.0	171	1	US-08-438-753B-30	Sequence 30, Appl
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OM protein - protein search, using sw model

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Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM protein - protein search, using sw model

Run on: September 9, 2006, 00:32:28 ; Search time 18.72 Seconds
(without alignments)
67.548 Million cell updates/sec

Title: US-10-797-626-3

Perfect score: 85

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	39	45.9	213	6	US-10-953-349-28900
8	39	45.9	213	7	US-11-056-355B-62667
9	39	45.9	216	6	US-10-953-349-30984
10	39	45.9	216	7	US-11-056-355B-67575
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